

FIGURE 1

CCAATGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCATGGCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTGTTCAAGAGCGTTCTGCTAATCTACACTTTATTTTC
TGGATCACTGGCGTTATCCTTCTGAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
CTTTCTCTTTAAATGAGAAGGCCACCAATGTCCCCTCGTGCCTACTGGTACCG
TCATTATTCTTGGAACCTTGGTTGTTGCTACCTGCCAGCTCTGCATGGATGCTA
AAACTGTATGCAATGTTCTGACTCTCGTTGGTCAACTGGTCGCTGCCATCGTAGG
ATTGTTTCAGACATGAGATTAAGAACAGCTTAAGAATAATTATGAGAAGGCTTGAAGC
AGTATAACTCTACAGGAGATTATAGAACCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGGTGGTGTACCGATTATAGAGATTGGACAGATACTAATTACTCAGAAAAGGATT
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTCCTTGGAGTTGCTGCTTCCAATGATTGAAATCTTCTGCCTACTGCCWCTCTCG
TGCCATAACAAATAACCAAGTATGAGATAGTGTTAACCCAATGTATCTGTGGGCCTATTCTCT
CTACCTTAAGGACATTAGGGTCCCCCTGTGAATTAGAAAGTTGCTGGCTGGAGAACTG
ACAACACTACTGATAGACCAAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGCTGAT
TCAATCAAGATGTATGTTGCTATGTTCTAAGTCCACCTTCTATCCCATTGTTAGATCG
TTGAAACCCGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT

FIGURE 2

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><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
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VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPKSCCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV
```

Important features of the protein:

Signal peptide:

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACCGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTGCCGTTCTCGGACCTGTCACAAA
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCGGGAGGGTAGAGAAAGTCAGT
GCCACAGCCCCACCAGCGCTGCTCTGAGCCCTGGGCACGCAGAACGGGAGGGAGTCTGAGGGT
TGGGGACGTCTGTGAGGGAGGGAACAGCCGCTCGAGCCTGGGGCGGGACCGGACTGGG
GCCGGGGTAGGCTCTGAAAGGGCCCAGGAGAGAGGGTAGGCTGGCCTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTCCACCGAGGCCGCGCTTGAGGGATCTGAAGAGGTTCTAGAAGAGGGT
GTTCCCTCTTCGGGGGTCTCACCAAGAGGTTCTGGGGTCGCCCTCTGAGGAGGCT
GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAAATCCCTGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTCTTGGCATTCAAGTTGTTAAAAACAAATAGGATGCAAATTCC
TCAACTCCAGGTTATGAAAACAGTACTTGGAAAAGTAACTACCTAAATGATCGTCTTG
GTTGGCCGTGTTCTAGCGAGCAGAACGCCTGGCCAGGGTCTGTTGACTCTCGAAGAG
CACATAGCCCACCTCCTAGGGACTGGAGGTGCCGCTACTACCATGGTAATTCTGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAACAGCAACAGGCCAGAACAGTG
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCTGTCGCCACCAAGGAGGGC
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAATGTGGATGGCTAGTGTGGACACACT
GGCAGTAATACGGACTCTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAAT
GAAAAGTGTCTGCCGGAACCATGACTTTAGGACTCCTCAGTCCTTAGGACATACTCG
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTAAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTGATGTTTGCTGCTGTACACTTGCTGGAAATGTCTAAATGTTTC
TGTAGCAGAAAACACGATAAAGCTATGATCTTATTAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKQNVGVLVDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

GGCACGAGGCGCTGCCACCCGGGGCGTGGGAGTGAGGTACCAAGATTAGCCCATTGGCC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTAACGGACTG
CAAGATGGAGGAAGGCAGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTCGTCTCAGGCTTCGCTTTCCGAAGC
CTTCCCCGACATACTTCGGACTAGTGCAGAGCAAACCTTCCCTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTGGCTCACAGCATGCTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCAGCTTACCTGCTGTTCTGAGCCTACGCTGCCACTGTCAAC
GCCCGCTGGCTGGAACCCCGACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGTGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCCTCCGCCAGAATTCTTCCGCTACCATGGGCTGTCC
TCTCTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCGCTGGCCTGCCCTGGA
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAAATGCTTCTCAGAAATGAAAAAAA
AAAAAAAAAAAA

FIGURE 6

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107
<subunit 1 of 1, 231 aa, 1 stop
<NX(S/T): 0
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GCAF INLC ILASQ HAWA QLT FW EAS QLY LLFLS LT LATVNARW LEPRTTAAMW ALQT VEKER
GLGGEVPGSHQGP DPYRQLRE KDPK YSAL RQNFF RYHGLSSLC NLGC VLSN GLCLAGLA LEIRSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCA GATTTAAGCCCATTCTGCAGTGGAA T T CATGAACTAGCAAGAGGA CACC ATCTT
 CTTGTATTATA CAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAA**TG**CTCTTTGGGT
 GCTAGGCCTCCTAATCCTCTGTGGTTCTGTGGACTCGTAAAGGAAA ACTAAAGATTGAAG
 ACATCACTGATAAGTACATTTTATCACTGGATGTGACTCGGGCTTGGAAACTTGGCAGCC
 AGAACCTTGATAAAAAGGGATTCATGTAATCGCTGCCTGTACTGAATCAGGATCAAC
 AGCTTAAAGGCAGAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG
 AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGAGAAAGGTCTCTGGGT
 CTGATCAATAATGCTGGTGTCCCGCGTGCTGGCTCCC ACTGACTGGCTGACACTAGAGGA
 CTACAGAGAACCTATTGAAGTGAACCTGTTGGACTCATCAGTGTGACACTAAATATGCTTC
 CTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAAATGTCTCCAGTGGAGGTGCCCTTGCA
 ATCGTTGGAGGGGCTATACTCCATCAAATATGCAGTGGAAAGGTTCAATGACAGCTTAAG
 ACGGGACATGAAAGCTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTAAAACAA
 ACTTGGCAGATCCAGTAAAGGTAAATTGAAAAAAACTGCCATTGGAGCAGCTGTCTCCA
 GACATCAAACAACAAATGGAGAACGTTACATTGAAAAAAAGTCTAGACAAACTGAAAGGCAA
 TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
 GTCTCTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAATTTCTGGATAACCTCTG
 TCTCACATGCCAGCAGCTTGCAAGACTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
 TCCCAAGGCAGTG**TG**ACTCAGCTAACCAACAAATGTCTCCTCCAGGCTATGAAATTGGCGAT
 TTCAAGAACACATCTCCTTTCAACCCATTCTTATCTGCTCCAACCTGGACTCATTTAGA
 TCGTGCTTATTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGCTCTG
 CTCAAGTTCTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT
 ATTTAGGCTTGCCTGCTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAATG
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FIGURE 8

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><MW: 35227, pI: 8.97, NX(S/T): 3
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ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCTIEPGLFKTNADPKVIEKKLAIWEQLSPDIKQQYGEFYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTGTTGACGGCGCTGCG**ATG**GCTGCCTGCGAGGGCAGGAGAACGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCCCTGACGCCGCCAGTGGCGGGGCCCTGGGCCGTGCCACCACT
 GTAGTCATGTACCCACCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGACGCTGAG
 CTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCCGCTCGTGCTGGAGGAAATGGA
 AGCAACTGTCGAGATTGACGGAAATATGATTCTCTCCTGCCTTCTGCTTTCTGT
 GGACTCCTCTTACATCAACTTGGCTGACCATTGAAAGCTCTGGCTTCAGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGTTAAAACCAGCAAATCCACCCGTCTACCAG
 CTCCCTCAGAAGGCCGACACCGACCCCTGAGAACTTACCTGAGATTTCGTACAGAACACAA
 AGACACATCCAGCAGGGGACACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA
 TGGGACCCAGGAGGAGGCCACAAAAAGGCAAGAACGGCCCTGTGGATCCCCGCCGAAGGAG
 ATCCGCAGAGGACAGTCATCAGCTGGAGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG
 CTCCCTCAAGAACAGAGCAGAAGTGCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG
 CACACCAGTGCATCTGAACATCGCCAGAAGGGCGTGATTGACGTCTCCTGCATGCATGGA
 AAGGATACCGCAAGTTGCATGGGCATGACGAGCTGAAGCCTGTGTCAGGTCTTCAGT
 GAGTGGTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCAGTGGATCTGGTCT
 GAGGAAAGAATTGAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTTACACTTGAAAAGGACG
 TGGACGTCAACCTGTTGAGAGCACGATCCGCATCCTGGGGGGCTCTGAGTGCCTACAC
 CTGTCTGGGGACAGCCTCTCAGGAAAGCTGAGGATTGAAATCGGCTAATGCCTGC
 CTTCAGAACACCATCCAAGATTCTACTCGGATGTGAAACATCGTACTGGAGTTGCCACC
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTGAGCTGGAGTTCCGG
 GAGCTCTCCGTCTCACAGGGATAAGAACGTTTCAGGAGGCAGTGGAGAACAGCA
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 GCCTCTCACCCACCTGGCGTATTACGCTGGCGCCAGGGCGACAGCTACTATGAGTAC
 CTGCTGAAGCAGTGGATCCAGGGCGGAAGCAGGAGACACAGCTGCTGGAAAGACTACGTGGA
 AGCCATCGAGGGTGTCAAGACGCACCTGCTGCGGCACTCCGAGCCCAGTAAGCTCACCTTG
 TGGGGGAGCTGCCACGGCCCTTCAGTGCCTAGAACGATGGACCACCTGGTGTGCTTCTGCCA
 GGGACGCTGGCTCTGGCGTCTACCACGGCTGCCAGCCACATGGAGCTGGCCAGGAGATCG
 GCTCATGGAGACTTGTACCAAGATGAACCGGCAGATGGAGACGGGCTGAGTCCCAGATCG
 TGCACTTCAACCTTACCCCCAGCCGGCGTCGGGACGTGGAGACCTGTTACCTGTACCGCGTCACAGGGGA
 CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTACCTGTACCGCGTCACAGGGGA
 CCGCAAATACCAGGACTGGGCTGGGAGATTCTGCAGAGCTTCAGCGATTCACACGGGTCC
 CCTCGGGTGGCTATTCTCATCAACAATGTCCAGGATCCTCAGAACGCCCAGCCTAGGGAC
 AAGATGGAGAGCTTCTCTGGGGAGACGCTCAAGTATCTGTTCTGCTTTCTCGATGA
 CCCAACCTGCTCAGCCTGGACGCCACGTGTTCAACACCGAACGCCACCTCTGCTATCT
 GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGACTTCGGGTGGCAGAGCACCTG
 CTGGGTCTGTCATTTCCAAGGGCCCACGTAGCACCGCAACGCCAACGTGGCCAGGCT
 CTGAACCTGGCTCTGGCTCCTCGTCTGTTAACAGGACACCGTGGAGGACAAGTGA
 GGCGTCAGTCTGGTGTATGCCGGTGGCTGGGCCCTGGAGCCTCCGCTGCTTCTC
 CAGAACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGCCGACCA
 GAGGGGGGCTCGAGGTGGTCCCTGGTACTGGGTGACCGAGTGGACAGCCCAGGGTGCAGC
 TCTGCCGGCTCGTAAGCCTCAGATGTCCCCAATCCAAGGGCTGGAGGGCTGCCGTGA
 CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTACAGCTGGACTCAGGGATCCTC
 CTGGCCGCCCGCAGGGGCTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGCCCCT
 CCAGTGGAAATGGGTCTTCTGGAGATAAAAGTTGATTGCTCTAACCGCAA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
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SKSWRRRSCWRWKQLSRLQRNMILFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSSRAEVPTKPLPPARTQGTPVHLNY
RQKVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFESTIRIILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAIVEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTLGVTL GARADSYYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLT FVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRDVEVKPADRHNL RPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFTRVPSSGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

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GGCGCCGCGTAGGCCCGGGAGGCCGGCCGGCCGGCTGCGAGCGCCTGCCCATGCGCCGC
 CGCCTCTCCGCACG**ATG**TTCCCCTCGCGGAGGAAAGCGCGCAGCTGCCCTGGGAGGACGGC
 AGGTCCGGGTTGCTCTCCGGCGCCTCCCTCGGAAGTGTTCGTCTTCCACCTGTTCGTGGC
 CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTAGCTGCTCTGGGACGTGG
 CCCGGCAGTCAGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCTAGAG
 CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT
 GCCCTTCCCGAACGCTTCGAGGAGCTCCTGGTCTCGTGCCTCACATGCGCCGCTTCCTGA
 GCAGGAAGAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACCTCAGGTTCAAC
 CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
 GCACGACGTTGACCTGCTCCCTCTAACGAGGAGCTGGACTATGGCTTCCTGAGGCTGGC
 CCTTCCACGTGGCCTCCCCGGAGCTCCACCCCTCTACCAACTACAAGACCTATGTCGGCGGC
 ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGATGTCCAACCGCTCTGGGG
 CTGGGGCCGCGAGGACGAGTTCTACCGGCGATTAAGGGAGCTGGCTCCAGCTTTCC
 GCCCTCGGAATACAACACTGGGTACAAGACATTGCCCCATGCTGACAGGCTGGCAGGGAGGG
 AAGAGGGACCAGAAGCGCATCGCAGCTAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG
 AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGACTGCCCTGTCTGTGGCGGGCCC
 CCTGCACTGTCCTAACATCATGTTGACTGTGACAAGACCGCCACACCCCTGGTGCACATT
AGCTGAGCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATTGCTCAGGCTCAGGA
 CAAGGCCTCAGGTCGTGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
 AGCTACGCAATTGCAAGCCACCCGGCCAAAGGCAGGCTTGGCTGGCCAGGACACGTGGG
 GTGCCCTGGGACGCTGCTGCCATGCACAGTGATCAGAGAGAGGCTGGGTGTGCCTGTCCG
 GGACCCCCCCTGCCTCCTGCTCACCTACTCTGACCTCCTCACGTGCCAGGCCTGTGG
 TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTCACGTGCC
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FIGURE 12

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RHIIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDV DLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDEFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAQKQEKFVDRREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCKTATPWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTGCCTATCCACCTCCCCAAGCCCCCTTACCTATGGCTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTAAAGGCTCATGCTGGAGTGGGACTGGTCGGGCCAGAAAGTCT
CTTCTGCCACTGACGCCCATCAGGGATTGGGCCTTCTTCCCCCTCCTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGT
GGGGGATGGCTAAGAAAGCTGGAGATAGGAACAGAAGAGGGTAGTGGGTGGCTAGGGG
GCTGCCTTATTAAAGTGGTGTTATGATTCTTACTAATTATAACAAAGATATTAAGGC
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FIGURE 14

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SQAQ
PRGEGEKVGDG
```

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGCAGGGACAAAG
GAGCATGTCCCGCGCCGGGAAGGCCCCTCGCTCCGGCCATAAGGCTCCGGTCGCCGCTGG
GCCCGCGCCGCGCTCTGCCCGCCGGCTCCGGGGCGGCCGCTAGGCCAGTGCGCCGCG
CTCGCCCCGAGGCCCGCCGAGC**ATG**GAGCCACCGGACGCCGGCGGGCCGCGCA
GCCGCCGCTGTTGCTGCCGCTCTCGCTTAGCGCTGCTCGCCTGCTGGGAGGCAGCG
GCGGCGGCCGCGCGCTGCCGCCGGCTGCAAGCACGATGGCGGCCCGAGGGGCTGG
AGGGCGGCCGGCGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACTCGCGCAGGTCT
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GACAAACAATCGAATAGGATGTCGAATGCAGACATATTCGAGGACTCACCAATCTGGTC
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GAATTGCCGTCTTCTACATGACTCCATCTCATGCCAAGTTGTGTTGAAGGAGACAGCCT
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GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTGTTGAAAAGAACATGATTACAAC
TGCTCCTGATTGCAAGTGCCTAACCATTTCTAATATTCAAGGCTGGATCTACTGGAATTG
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ACTTTCGGATTATGGGAGGCGGGATCCAGAGGGAAACCTGGATAAGCAGCTGAGCTTAAAGT
GCAATGTTCAAATACATTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATT
AAGACTATTACAGT**TAA**ATTAGAATGCTCCAAATGTTCTGCTCGAAAATAACCTTATT
AAAGATTTTTTGAGGAAGATAGGTATTGCTTTGCTACTGTTAAAGAAAACAA
ACCAGGAAGAACTGCATTACGACTTCAAGGGCCCTAGGCATTTGCTTGTGATTCCCTT
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ATTGTTACATGTGAAAAAATTGACTTAAAGTTATTGTTATTGTTTTGCTCCT
GATTTAAGACAATAAGATGTTCTGGCCCTAAAGTATCATGAGCCTTGGCACTGC
GCCTGCCAAGCTAGTGGAGAAGTCACCCCTGAGACCAGGTGTTAATCAAGCAAGCTGTAT
ATCAAATTTGGCAGAAACACAAATATGTCATATCTTTTAAAGTATTCA
TTGAAGCAAGCAAATGAAAGCATTACTGATTAAAGATTGGTGTCTTAGATATATT
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TACTTATTCTGTCTGTCCTCAATAATATCACAAACAATTCCAGTCATTAAATGGC
TGCATAATAACTGATCCAACAGGTGTTAGGTGTTAGTGTGAGCACTCAATAAA
TTGAATGAATGAACGAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRGRAQPPLLPLSLLALLALLGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
VVCSSLELAQVLPPDTLPNRTVTLLSNNKISELKNGSFSGLSLLERLDLRRNNLISSIDPGA
FWGLSSLKRDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLEFQT
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLTCDPPELPSFYMTP
SHRQVVFEGDSLPCQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT
ISNIQAGSTGNWGCHVQTKRGNNRTVDIVVLESSAQYCPPERVVNNKGDFRWPRLAGITA
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGFWADDYSRCQYANDVTRVLYMFNQMPLNL
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEKSKELGDVMDIASNIMLA
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
VFQKVAASDRTGLSDYGRRDPEGNLDKQLSKFCNVNTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
384-390, 403-409, 554-560

FIGURE 17

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGTGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATTGGAAAAAGAAAACATTGCTTTGGGAGAACAGATTA
TTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTAAAAAA
TCATGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTGTGTGTGTTGAT
GGAGAGTAGCTTAGTATCTTCATCTTTTTGGTCACTGTCCTTTAAACTTGATCA
AATAAAGGACAGTGGTCATATAAGTTACTGCTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGCAGACACTTTGGAAGAGTCTGTCGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTACTGAGAACACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAAC
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

FIGURE 18

MSRSSKVVLGLSVLLTAATVAGVHKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

FIGURE 19

CTGTCGTCTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTT
 CAAGTGTGGCTTAATCCGTCTCCACCACCAAGATCTTCTCCGTGGATTCCCTCTGCTAAGACC
 GCTGCC**ATG**CCAGTGA CGGTAAACCGCACCACCATCACAAACCACGACGT CATCTCGGG
 CCTGGGGTCCCCCATGATCGTGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC
 CTGCTGCAGCTGGTGTCTACCTGC GTGGC TTCTCGCTGGTGGCTAGCGTGGCGCCTGGAC
 GGGGTCCATGGCAACTGGTCCATGTTCACCTGGTGCTCTGCTTCTCGTGACCCGTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC
 ATCACCTTCGCCTGCTATGCGGCCCTTTCTGCCTCTCGGCCTCCATCATCTACCCCACAC
 CTATGTCCAGTTCCTGTCCCACGGCCGTTCGCGGGACCACGCCATGCCGCCACCTTCTTCT
 CCTGCATCGCGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGCCGGCCGGCGAG
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG
 CATCATCTTCGCGTTCATCGGACCCAACCTGTACCAGCACCAGCCGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATCTGCTTACCGCCATGCCATCCTGCTGAACCTGGGG
 GAGTGCACCAACGTGCTACCCATCCCCCTCCCCAGCTTCTGTGGGGCTGGCCTTGCTGTC
 TGTCCCTCTATGCCACCGCCCTTGTCTCTGGCCCTCTACCAGTTGATGAGAAGTATG
 GCGCCAGCCTCGGCCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCCTACTACGTGT
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
 TGACCTGGTGCACTCTGCCACCTGGTTTTGTCAAGGT**TAA**ACTCTCCAAGAGGCTCC
 CGTTCCCTCTCCAACCTTTGTTCTTGTGGCCGAGTTTCTTATGGAGTACTTCTTCC
 TCCGCCTTCCCTGTGGGGCTTCTGCTCCCTCCACCTTTCTTCCCT
 CAATTCCCTGCACTCTAACCAAGTCTGGATGCATCTTCTTCCCTTCTGCTGT
 TTCCTTCTGTGTTGTTGCCCACATCCTGTTTCAACCCCTGAGCTGTTCTTT
 CTTTCTTCTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCCTCTGGTTCAAGCGATTCTCCTCC
 CCCAGCCTCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTCT
 TTCCACTCTCTTTCTCATCTCTTCTGGGTTGCCGTGCGCTTCTTATCTGCCTGT
 TTTGCAAGCACCTCTCCTGTGTCCTGGAGCCCTGAGACTTCTCTCCTGCCTCCA
 CCCACCTCAAAGGTGCTGAGCTCACATCCACACCCCTGCAGCCGTCCATGCCACAGCCCC
 CCAAGGGGCCATTGCCAAAGCATGCCCTGCCACCCCTCGCTGTGCCTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTTGGGGGTGGGGGTGGTAGCTGGGATTGGCCCTCTTCT
 CCCAGTGGAGGAAGGTGTGAGCTACTTCCCTTAAATTAAAAACATATATATATAT
 ATTGGAGGTCAATTCCAATGGCGGGAGGCATTAAGCACCGACCCCTGGTCCCTAGG
 CCCGCCTGGCACTCAGCCTGCCAGAGATTGGCTCCAGAATTGGCCAGGCTACAGAACAC
 CCACTGCCTAGAGGCCATCTAAAGGAAGCAGGGCTGGATGCCTTACCCAACTATTCT
 CTGTGGTATGAAAAAG

FIGURE 20

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVRTTITTTSSSGLSPMIVGSPRALTQPLGLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTЛИLIVELCGLQARFPLSWRNFPITFACYAALFCLSASIYPTTY
VQFLSHGRSRDHAIАATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLетFVACI
IFAFISDPNLYQHQPALEWCVAVYАICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRLAVAILTAINLLAYVAD
LVHSAHLVFKV
```

Important features:

Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 21

GAACGTGCCACCATGCCAGCTAATTGGTATTTAGTAGAGACGGGGTTTCAACCAGTGGCCAGGCTGGTC
 TTGAACCTCGTACCTCATGATCCGCTCACCTCGGCCTCCAAAGTGCTGGGATTACAGGCATGAGCCACTGACGC
 CTGCCAGCCTATGCATTAAAGAAATTATTCTGTATTAGGTGCTGTGCTAACATGGCACTACAGTGACCA
 AACAGACTGAATTCCCCAAGAGCAAAGACCAAGCAGTGAGGGAGACCAACAAGAAACAGGAATGCAAAAGAGACCA
 TTATTACTCACTATGACTAAGGGTCACAAATGGGTACGTTGATGGAGAGTGATTTGTTAAGAGACTACAGAGGG
 AGGACAGACTACCAAGAGGGGCCAGGAAAGCTCCTGACGAGGTGGTATTCAAGCCAAACTGGAAGAATGA
 GAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGAGCACTACACTCACTACACTTGGCCTGAGAA
 AATAGCATGGATTGGAGGAGCTGGGGAACACCCTTCTGCCACCTGGGAGGCACTGGGAGGAGGAGGCTTGAGA
 AAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGAGCAGGGACTTGCAGGTGGAATCATTAGGTCTTATC
 AACAGATATGGGCAAGCAAAGCCAGGGAGAATTGATGTTAATGCTGAGGTTGGAGGCCAGGCTAGATGGACAG
 TGGTGGGTGATGCAAAGGAAAGAGGTCAAGGAAGCAGGGCAGACGTGGGAGAAGGTGTGGGGTTGGTTCCA
 TCTTGCAGTCTGCCGAATGTGGATGGGAAGACCAAGAGGGAGGAGCAAGGGCAGAGGGGAAGGGAATCTAA
 AGAAGTCCTGGATGCCACACTCTTCTCCTCTCCCTCAGAGGTCTCACTCGTGGTCTCAT
 TTCCTGCCCTGCCTCCATCTCCTGGGTGCTGGGAAAGTGGAGGATTAGCTGAAGTTGCTTCTCGGGGCTG
 TCTGAATCTCATTGCTTCTGGGAGGACATAATTACCTGCTCTAGCTTATCATCTTACATTCCCTGTAG
 CCACTGGGACATATGTTCTCTAGCTCCTGTCTCCCTCATGCCTTGCTGGTATGGCATGTTAG
 GGGGAAGGTATTGCTGTCAAGAGGGCACTGACTTTCTAATGGTGTACCCAAGGTGAATGTTGGAGACACAGTC
 GCGATGCTGCCAAGTCCCAGGCTAAGTCCAGGAGATCGTGCCTGGCAGGTCCCTGCATGGT
 ATGCAGCCCCCTCCC**ATG**TTCTGGCAGCTTGTCTTCTCCCTGCAGGTGAATCTCAGCCCTCTCCACCCAAAGGTTC
 ACATGGATCCTAACTACTGCCACCCCTCCACCTCCCTGACCTGTGCTCCCTGGCCTGGTCTTACCAAGGCTTC
 TCCACCCCTCCCTATCTCCAGGTATTCCCAGGTGGTGAAGGACCAAGTGAACAGCCTACGCCATGGCCAGG
 GCCGAGTGGCTCACCTCATTGAGTGGAGGGCTGGAGCAAGCCAGTGACTCACCTGCTGCCCTGGAATCAGCCT
 TTTCTCTTATTCAGACCTCAGCGAGGGCAACAAAGAGGTGCTGGCAGCAGGAGTGGCTGAGCAGTTGCCA
 TCGCGGAAGCCAAGCTCGAGCATGGTCTCAGGTGGATGGCGAGGACTCCACTGATGACTCTATGATGAGGACT
 TTGCTGGGGATGGACACAGACATGGCTGGCAGCTGCCCTGGGCCGACCTCCAGGACCTGTTACCGGCC
 ACCGGTTCTCCGGCTGTGCCAGGGCTCGTGGAGCCTGAGAGCGACTGCTCACAGACCGTGTCCCCAGACA
 CCCTGTGCTCTAGTCTGTCAGCCTGGAGGATGGTTGTTGGCTCCCCGGCGCTGGCTCCCAGCTGCTGG
 GCGATGAGCTGCTCTGCCAAACTGCCAGGGAAAGTGCCTTCCGAGCTGGCCACTGGAGGCC
 AGGACTCACTACAACACTGCCCTCACAGAGTCCTGCCCTCCCCCGGGAGGAGGAGGCCAGCCCCCTGCAAGG
 ACTGCCAGCCACTCTGCCACCACTAACGGCAGCTGGGAACGGCAGCGGCAAGCCTGACCTGCCCTTCTG
 GGGTGGTGTCTTAGATGAGGATGAGGCAGAGGCCAGAGGAACAG**TGA**CCCACATCATGCCCTGGCAGTGGCATGCA
 TCCCCCGGCTGCTGCCAGGGCAGAGCCTCTGCCCCAAGTGTGGCTCAAGGCTCCAGCAGAGCTCACAGCC
 TAGAGGGCTCTGGAGGGCTCGCTCTCCGTGTTGATGAAAGTGTGGAGAGGGAGGCCAGGGCTG
 GGCTGGGGCGCATGTCCTGCCCTACTCCGGGCTTGGCGGGGGTGGCCGGGCTCTGGGCATGGCTACA
 GCTGTCAGACAGTGATGTTCATGTTCTAAATGCCACACACATTTCTCTCGGATAATGTGAACCACTA
 AGGGGTTGTGACTGGCTGTGAGGGTGGGGTGGGAGGGGCCAGCAACCCCCCACCCTCCATGCCCTC
 TCTCTCTGCTTTCTCTCACTTCGAGTCATGTGCACTGCTGTTGATAGAATCACCCCCCACCCTGGAGGGCTGG
 CTGCCCTCCGGAGCCTATGGTTGAGCCGCTCCCTCAAGGGCCCTGCCAGCTGGCTCGTGTGCTGCTTC
 ATTACACTCTCCATCGTCTAAATCTCTCTTTCTAAAGACAGAAGGGTGGCTGGGCTCTGGCTCTGGCT
 GGATCTCTCTCTGGAGGCTTGGGAATGATGAAACCATGTAACCTCCACCCCTTCTGGCCCCCTAATGG
 GGCCTGGGCCCTTCCACCCCTCTAGGATGTGCGGGCAGTGCTGGCGCTCACAGCCAGCCGGGCTGCC
 ATTACCGCAGAGCTCTGAGCAGGGAGGTGGAGAAAGGATGGCTCTGGTGTGCAAGCTGATGCCCTGCTGAGAGGCAGGAAT
 CTTCTAGAGAGGGCCACAAGAGGGCACAGGGTGGCAGGAGTTGTCAGCTGATGCCCTGCTGAGAGGCAGGAAT
 TGTGCCAGTGAGTGACAGTCATGAGGGAGTGCTCTCTGGGAGGAAAGAAGGTAGAGCCTTCTGCTGAAT
 GAAAGGCCAAGGCTACAGTACAGGGCCCCGCCAGCCAGGGTGTAAATGCCACGTAGTGGAGGCCCTGGCAG
 ATCCTGCATTCCAAGGTCACTGGACTGTACGTTTATGGTTGTTGGAGGGTGGCTTGAATTAAGGGC
 CTTGTAGGCTTGGCAGGTAAAGAGGGCCAAGGTAAGAACGAGAGGCCAACGGGACAAGCATTCTATATATAAGT
 GGCTCATTAGGTGTTATTTGTTCTATTAAGAATTGTTATTAAATAAATAAAACTTTGTAATCTC
 TAAAA

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSFSHPKVHMDPNYCHPSTSLHLC
LAWSFTRLLHPPPLSPGI SQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPALESAFSSY
SDLSEGEQELEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
PHLQDLFTGHRSRPRQGSVEPESDCSQTVPSPDTLCSSLCSLEDGLLGSPARLASQLLGDE
LLLAKLPPSRESAFRSLGPLEAQDSLYNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTCCTGGCGCTGTTACACAAGCAAGATAACGCCAGCCCCACCTAATTTGTTCCCT
 GGCACCCTCCTGCTCAGTGCGACATTGTACACTTAACCCATCTGTTTCTCTAACGACGA
 CAGATTCCCTTCAGACAGGACAACGTGATATTCAAGTCTGATTGTAAATACCTCCTAACG
 CCTGAAGCTCTGTTACTAGCCATTGTGAGCTCAGTTCTCATCTGCAAAATGGGCATAA
 TACAATCTATTCTGCCACATCAAGGGATTGTTATTCCCTTAAAAAAACCAATACCAAAG
 AAGCCTACAATGTTGGCCTAGCCAAAATTCTGTTGATTCAACGTTGTTTATTCACTTCT
 ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACAGAACATTGCAGAAGTT
 TTAAAACAATGGAAAATAACCTATTCTTGAAAGTGAAGCAAACCTAAACTCAGATAAA
 GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCCTTGAATCTACCCAACAA
 CAGGCCACGGAATAACAGATTCTCCAGTAACTCATCAGCAGAGCATTCTGGCAGTCTAA
 AACCCACATCTACCATTCCACAAGCCCTCCCTGATCCATAGCTTGTCTAAAGTGCCT
 TGGAATGCACCTATAGCAGATGAAGATCTTGCCTCATCTCACGACATCCAATGCTACACC
 TGCTCTGTCTTCAGAAAACCTCACTGGTCTTGGTCAATGACACCGTGAAAACCTCTGATA
 ACAGTTCCATTACAGTTAGCATCCTCTTCAGAACCAACTCTCCATCTGTGACCCCTTG
 ATAGTGGAACCAAGTGGATGGCTTACACAAACAGTGATAGCTTCACTGGTTACCCCTTA
 TCAAGAAAAACAACTCTACAGCCTACCTTAAATTACCAATAATTCAAAACTCTTCCAA
 ATACGTAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTGGGCCATTAGGT
 GCTATTCTGGGTGTCATTGCTACTCTTGTGGCTACTGTTGTGGAAAAAGGAAAAC
 GGATTCAATTCCCCTCGCGACTTATGACGACAGAAATGAACCAAGTCTGCGATTAGACA
 ATGCACCGAACCTTATGATGTGAGTTGGAAATTCTAGCTACTACAATCCAACCTTGAAT
 GATTAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATCCTATGGATGACATACC
 TCCACTTCGTAACTAGAACTAACAGCAAAAGGCCTAACAGCAAGTGTCTAC
 CATCCTAGCCTTTGACAAATTCACTTTCAAAAGGTACACAAAATTACTGTCACGTGGAT
 TTTGTCAAGGAGAATCATAAAAGCAGGAGACAGTAGCAGAAATGTAGACAGGATGTATCAT
 CCAAAGGTTTCTTACAATTGGCATCCTGAGGCATTACTAAGTAGCTACCTTAATT
 TGTATTAGTAGTATTCTTAGTAGAAAATATTGTGGAAATCAGATAAAACTAAAAGATT
 TCACCAATTACAGCCCTGCCTCATAACTAAATAATAAAAATTATTCCACCAAAATTCTAAA
 ACAATGAAGATGACTCTTACTGCTCTGCCTGAAGCCCTAGTACCATATTCAAGATTGCAT
 TTTCTTAAATGAAAATTGAAAGGGTGTGTTAAAGAAAATTGACTAAAGCTAAAAGAG
 GACATAGCCCAGAGTTCTGTTATTGGAAATTGAGGCAATAGAAATGACAGACCTGTATT
 TAGTACGTTATAATTCTAGATCAGCACACATGATCAGCCACTGAGTTATGAAGCTGA
 CAATGACTGCATTCAACGGGCCATGGCAGGAAAGCTGACCCACTACCCAGGAAAGTAATAGCT
 TCTTAAAGTCTTCAAAGGTTGGAAATTAACTTGTCTTAATATATCTTAGGCTTCAA
 TTATTGGGTGCCTTAAAACCTCAATGAGAATCATGGT

FIGURE 24

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTSNDSFTGFTPYQEKTTLQPTLKFTNNSKLFPNTSDPQKENRNTGIVFGAILGAIL
GVSLLTLVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNSA
MPESEENARDGIPMDDIPPLRTSV
```

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCGAAGATTCACT**ATG**TGAAAATCGCCTTCATAACCCCTACCGCCGTGAAAAGGGAGG
 AGGCACGGCAAGACGTGGAGGCCCTCCTGAGCCGACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTGCACCCAGGAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCTTCATTCATCTGGCAGGACTTATTGTTGGAGCCTGCATTACAAGTACT
 TCATGCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTGATTCTGAGGATCCTGCA
 AATTCCCTCGTGGAGGAGAGCCTAACCTCCTGCCTGTGACTGAGGAGGCTGACATTGTGA
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTCTGTGATAGTGACCCCTGCAG
 CAATTATTGACTTTGAAAAGGAATGACTGCTTACCTGGACTTGTGCTGGGAACTGC
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTTTGG
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTCAGAGAACCTAGTTGCTG
 TGGAGGAAATTGATGTTAGTAACCTGGCATCTTACCAACTTGCAATAACAGA
 AAGTCCTTCCGCCTCGTCGCAGAGACCTCTGCTGGTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTATTGTTGAGACCAAGATCTGTCAAGAG**T**
AAGAGGCAACAGATAGAGTGCCTGGTAATAAGAAGTCAGAGATTACAATATGACTTAA
 CATTAAGGTTATGGGATACTCAAGATATTACTCATGCATTACTCTATTGCTTATGCTT
 AAAAAAAGGAAAAAAAAAAACTACTAACCAACTGCAAGCTTGTCAAATTTAGTTAAT
 TGGCATTGCTTGTGAAACTGAAATTACATGAGTTCATTGCTTGCATTATAG
 GTTTAGATTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCCATCC
 GTTGTGTTGTTGTTGTTGTTCTTCTTAAAGTAAGCTTATTGATCTTATGCTT
 GTGGAGCAATTAAAATTGAAATATTAAATTGTTGAACTTTGTGAAATATA
 TCAGATCTCAACATTGTTGGTTCTTGTGTTCAATTGCTTGTACAACATTCTGAAATTAGA
 AATTACATCTTGCAGTTCTGTTAGGTGCTCTGTAATTAAACCTGACTTATATGTGAACAAATT
 TTCATGAGACAGTCATTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTAGGTGATGAATTCTACAA
 CCCTATAATAAATTACTCTATACAAAAAAA

FIGURE 26

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
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<MW: 29741, pI: 5.74, NX(S/T): 1
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ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPAANSLRGEPNFLPVTEADIREDDNIA
IIDVPVPSFSDPAAIIHDFEKGMTAYLDLLLGNCLMPLNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIFYQLCNNRKSFRRLRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCCAGCCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT
 CTTCCAGCCCAGGTGCCCTTCACTCTCGCTCCATTGGCGGGAGCACCCAGTCCTGTACGCC
 AAGGAACCTGGTCTGGGGCACC**ATG**TTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGAGGCCAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC
 CGCCACCCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGCCAGCCCACAACCCCTGGGG
 GCCCATCACCCCCCACCAACTCCTGGATGGGATAGTGGACTTCTCCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTCTGCTGATGTTCATCGTCTGTGCCCGGTCA
 TCACCCGGCAGAACGGCAGAACGGCCTCGGCCTATTACCCATCGTCCTCCCCAAGAACAGTAC
 GTGGACCAGAGTGACCGGGCCGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCGAGGAAGCCCTGGATTCCCTCCGGCAGCTCCAGGCCAGATCTGGCCG
 CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGCGGTGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGCGCAGAGGAAGAGGAGAACGGCAGCCAGGAGGGGACCAGGAAGTCCA
 GGGACATGGGGTCCCAGTGGAGACACCAGAGGCCAGGAGGAGCCGTGCTCAGGGTCTTG
 AGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTGTTAGCCAG
 GAAGCCCAGGGACCAGTGGTCCCCCGAAAGCCCTGTGCTTGAGCAGTGTCCACCCAG
 TGTC**TAA**CAGTCCTCCGGCTGCCAGCCCTGACTGCTCCTGACACTCCCTCCTGGCCTCC
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTCCTGACACTCCCTCCTGGCCTCC
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTCCCCGG
 GGAATCTTACCAAGTGCCATCATCCTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
 ACAGCTCCCTGACAAAGTGAGGGAGGGCACGTGTCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGCTGGATTACAGCGTGAGCCACCGTGCCGGCCAAACTACTTTAAAACA
 GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTC
 TGGCCCCCTGTTCTAGTTGGTCCAGGATTAGGGATGTGGGTATAGGGCATTAAATCCTC
 TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGTGAGTTCTCATCCCGCTACTGCTGCTGG
 GATCAGGGTTGAATGAATGGAACCTTCCCTGTCTGGCCTCAAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTGAGGGACCTCCACCCCTGGGAAGTCCGAGGGCTGGGAAGGGTTCTGACG
 CCCAGCCTGGAGCAGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGCTGGCAGCCTG
 TGTCCACAATATTGTCAGTCCTCGACAGGGAGCCTGGCTCCGTGCTTCTGTTAGGGAGGCT
 CTGGCAGGGAGGTCTCTCCCCCATCCCTCCATCTGGGCTCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAGCACAATAAACCTTATTCCGGCCTGAAAAAAAGA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pi: 4.52, NX(S/T): 0
MVSAAAPSLLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEGLSSASSPSLPPWTPAL
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEKGSQEGDQEVTQGHGVVPETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLQAQEAQGPVGPPESPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAAGGCTGCAGACCCAGAGGGA
 GGGAGGACAGGGAGTCGGAAAGGAGGAGCACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
 GCAAGGAGGAGACCCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGCTGGCAGAG**ATG**
 AAGTTCCAGGGGCCCTGGCCTGCCTGCTGGCCCTGCTGGCAGTGGGAGGCTGG
 CCCCTGCAGAGCGGAGAGGAAAGCACTGGACAAATATTGGGGAGGCCCTGGACATGCC
 TGGGAGACGCCCTGAGCGAAGGGTGGAAAGGCCATTGGCAAAGAGGCCGGAGGGCAGCT
 GGCTCTAAAGTCAGTGAGGCCCTGGCCAAGGGACCAGAGAACAGCAGTTGGCACTGGAGTCAG
 GCAGGTTCCAGGCTTGGCGCAGCAGATGCTTGGCAACAGGGTCGGGAAGCAGCCCAG
 CTCTGGAAACACTGGCACGAGATTGGCAGACAGGCAGAAGATGTCAATTGACACGGAGCA
 GATGCTGTCGGCCTGCTGGCAGGGGTGCCTGCCACAGTGGTGCCTGGAAACTCTGG
 AGGCCATGGCATCTTGGCTCTCAAGGTGGCCTGGAGGCCAGGGCAATCCTGGAG
 GTCTGGGACTCCGTGGTCCACGGATAACCCGGAAACTCAGCAGGCAGCTTGGAAATGAAT
 CCTCAGGGAGCTCCCTGGGTCAAGGAGGCAATGGAGGCCACAAACTTGGACCAACAC
 TCAGGGAGCTGTGGCCCAGCCTGGCTATGGTCAGTGAGAGGCCAGCAACCAGAACATGAAGGGT
 GCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGAGGCAGCGGC
 TCACAGTCGGGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGG
 TGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCCTGG
 TCCAGCACCGGCTCCTCCGGCAACCACGGTGGAGCGGGAGGAAATGGACATAAAC
 CGGGTGTAAAAGCCAGGAATGAAGCCCGGGAGCAGGGAAATCTGGATTAGGGCTTCA
 GAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGCCATCGCCTGG
 GGCTCTGGAGACAATTATCGGGGCAAGGGTCAGCTGGGCAGTGGAGGAGGTGACGCTGT
 TGGTGGAGTCAATACTGTGAACCTGAGACGTCTGGATGTTAACACTTGTACACTTCT
 GGAAGAATTAAATCCAAGCTGGTTCATCAACTGGGATGCCATAAACAGGACCAGAGA
 AGCTCTCGCATCCCG**TGA**CCTCCAGACAAGGAGGCCACAGATTGGATGGAGCCCCACACT
 CCCTCCTAAACACCACCCCTCTCATCACTAACTCAGCCCTGCCCTGAAATAACCTTA
 GCTGCCCAACAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAA

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLGGQGQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSCGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSGSSGSSGGSSGGSSGGSSGSGSNGSGSRGDSGSESSW
GSSTGSSSGNHGSGGGNGHPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL
GGSGDNYRGQGSSWGSGGDAVGGVNTVNSETSPGMNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGGTCCCTCCGGTCTGGATGTCCGGACTCTGCTGCAGCGAGGGCTGCAGGCCGCCGGCGGTGCTCACCG
 TGCCCTGGCTGGAGTTCTCCTCTGGTCTGACCATGTTGTTCCCTGCTGGAATATTACCGGGACATCTTCA
 CTCTCCTGCTGCCCTGCACCGGAGCTTGGTGTGTCGAGGAGACTGAGGGAAAG**ATG**TGTTCTGAACAAGC
 TGCTGCTACTTGCTGCTGGCTGGCTTCCAGATTCCCACAGTCCCTGAGGACTTGTCTTCTGGAAGAGG
 GTCCCTCATATGCCCTTGAGGTGGACACAGTAGCCCCAGACATGGCTGGACAATGCGCCTGTGGTGGACCAGC
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGAAACTGCTCGCTCGTGGGTGTCAGGCAGTAGTG
 GACGGAGTGGGGCTTCATGAGGAAATCACCCCCACCACTACACCACGCCCTGGGAGGCCAGCCTCCCAGACCA
 GCCAGGGCTGCAAGCACAGCTGCCAGGCCCTTTCCACAACCAGCCGCCCTTGCCGGACCGTAGAGT
 TCGTGGCAGAAGAATTGGATCAAACACTGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGCAGCAG
 CAGAGTCACTCTCCAAGAGCAGCTGGTACACAGGGAGAGGAAGGGGAGACCCAGCCAGCTGGAGATCT
 TGTGTTCCCAGCTGTGCCCTCACGGGCCAGGCATTGCCCTGGGGGGAGCTGTCAAAGGAAGGCCCTG
 GGGCTGTGCCGGCGCTGCTCCAGAGGAGACCCCGCAGCCGTTCTGAGCAGTGCAAGAGAACATTGCTGTGGGC
 TTGCAACAGAGAAAGCCTGTGCTGGCTGTGACCCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG
 TGAGTCGCACACTCGAGCCAGGGCCTGTGACCTGCTGCCGGGGAGCGGAGGGGCTGCTCCCGCC**TGAC**
 GTGCTCTCTGGCCGTGGGGCACGGGACCTGACGAGGGAGTCTCCCAGAGCATTGGAACAGCTCCTAGGC
 CAGCTGGGCCAGCAGCTGCCAGTCCCTGTGCCACCTGCTGAGCAGCATTGCAAAGTGTCTGTG
 GAGTTAGCTCCCTCTCGTGCAGATCAAATTCTATCCTAGGGCCCCCGCACAGTACAGGCTGGAGAGAGGG
 CAGGCTCGAAGGCTCTGACATGCTGCTTCTGTGAACTGCTGCCGGGGAGCGGAGGGGCTGCTGCCAGCTG
 CTGCTGAGCCAAGAAATGTGGGGCTCTGGCAGACACAAGGCCAACGGAGTGGACTTGTCTGCTATTCTGCTA
 CGGGAGCTGGTGGAGAAGGGCTGATGGGACGGATGGAGATAGAGGCCCTGCCCTGGCAGCCTCCACCAGGCCAG
 TGGCCAGGGACTTGCTGAAGAATTAGCAACACTGTCTAATCTGTTCTAGCCGAGCCCCACCTGCCAGAACCC
 CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGCCAGAGCTAGGGCTGAGAAGTGGCC
 CTGCTTGGCATTGACCCAGAACCTGGACCCCCGCCTACGAGGAGGCCAACGGAGTGGACTGCCAATGCAAGACCC
 TGTTGGGGTAGCTGGTCTACAGTCAGACTCTGCTCTAAGGGTGTCACTGCCATCCCACCGCGA
 ATCCTAGAGGAAGGAGAGTTGGCCTGATTGGGATTATGGCAGAAAAGTCCAGAGATGCCAGTCCTGGAGTAGAA
 GAGGTGGTGTGTTATCTCTGGATACTAAATGAAATGAGGTGTGCTGGCTGTCAACACAGAACATTCAAGCCT
 CATTTGCTATCCCAGCATCTCTTAAACTGTGAGTCTTGGAAATTCAACAGAGGCCAAATGACTCCTGCTTAAC
 TTATGAAGAAAGTTAAACATGAATCTGGGAGTCTACATTCTTATCACAGGAGCTGGACTGCCATCTCCTT
 ATAAATGCCAACACAGGCCGGCTGGCTCATGCCGTAAATCCCAGCATTGAGAGGCCCTGAGGTGGCG
 GACTGCCAGGTCAAGGCAATTCAAGACCAGCCTGGCAACATGGAAAACCCCATCTCTACTAAAAATAAAAAA
 TTATTAGCTGGCATGGTGGTGTGCTGTAAATCCCAGCTACTCAGGAGGAGTGGCAGGAGACCTGCTTGAAC
 CTGGAGGTGGAGGTTGCACTGAGCCAGGTCGACCACTGCACTCCAGTCTGGTAACAGAGCGAGACTTCTAG
 AAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTCCCCCTGTACCTTCAGCCCTG
 TGCAGGTAGTAACCTCTTGAGACCTCCCTGACCAGGGACCAAGCACAGGGCATTAGAGCTTTTAA
 CTGGTTTCTTAAAAAAAAAAGGGCTTTATTAAATTCTCCCCACAGATGGCTCTGCAATCTGCCACAGCTC
 TGGGCGTGTCTGTAGGGAAAGGCCCTGTTTCCCTGAGGCGGGCTGGCTGTCCATGGTCCGGAGCTG
 GCCGTGCTGGCGCCCTGGCGTGTGCTAGCTGCTTCTGCGGGCACAGAGCTGCCGGCTGGGGCACCAGGG
 AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCCCTGCTCTTAAACCGACACCCCTGAGGTGCTCTGAGATGCTG
 GGTCACCCCTGAGTGGCACGGGGAGCAGCTGTTGGCGGTGCTCCTCYTAGGCCAGTCTGGGGAAACTAAGCTC
 GGGCCCTTCTTGCCTGGGAGGATGGGGTGGGTGAGGGACTCATGGGAATGCCCTGAGGAGCTACGTG
 GAAGAGGGCGCCGGTTGGCTGAGGCCCTGGAGGCCCTCTCCTGAGGCTCAGTTCCCTTCCGTCTA
 ATGAAGAACATGCCGTCTGGTCTCAGGGCTATTAGGACTTGGCCCTGGCACGTGAGGCTTGGACAGCGTCA
 GTTATTTCAACAACGTCTGCGACGTTGGCTGGCACGTGAGGCTTGGCACGAGCTGCGCTGGGGT
 GTCGCGGTGGAGTGGCAGGCCAGGGGGCCAGACGGTGCCTGGGGTGGAGGGAGGCGCCCCGGAGGG
 CCTCACAGGAAGTGGAGGCTCCGCACCAACAGGCAGGGGGCTCCGCCGCCGCCACCACCGTCCAGG
 GGCCGGTAGACAAAGTGGAGGCTGGCTCGCTGCGCAGCAGGTAGCCCTGATGCAAGTGCAGGCGC
 TCGTCCGCCAGCTGGAAGCAGGCCGTCCACAGCACGAACAGCCGGTGCCT

FIGURE 32

MCFLNKLLLLAVLGWLFOIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
CPYIGELRKLLASWVGSSGRSGGFMRKITPTTTSLGAQPSQTSQGLQAAQLAQAFFHNQPP
SLRRTVEFVAERIGSNCVKHIKATLVADLVRQAESLLQEQLVTQGEEGGDPAQLLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microparticles C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTCGGGTCTACTGAAGGCTGTCTGATCAGGAAACTG
 AAGACTCTCTGCTTTGCCACAGCAGTCAGCTCAGCTTGCAGCTTGCAGGAGAACCACATCCC
 TGCCCCCAGGGCACCTGCAGGACGCCACACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**
 AGTAGCAACAAAGAGCAGCGGTCAAGCAGTGTGATCCTCTTGCCCTCATCACCATCCT
 CATCCTCTACAGCTCAAACAGTGCCTGAGGCTTCCATTACGGCTCCCTGCGGGGCGTA
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC
 AACAAAGACACTGCCCTCTCGGTGCCACCAGTGTGATTGTCAGCAGCTCAGCCACCTGCT
 GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGATACAATCCGATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGCAACAAGACCACCTACCGCTGGCCATTCC
 AGTGTGTTCCGCGTGTGAGGAGGCCAGGAGTTGTCAACCAGGACCCCTGAAACCGTGT
 CATCTTCTGGGGGCCCGAGCAAGATGCAGAACAGCCCCAGGGCAGCCTCGTGCATGATCC
 AGCGAGCGGGCTGGTGTCCCCAACATGGAAGCATATGCCGTCTCTCCGGCGATGCGG
 CAATTGACGACCTCTCCGGGTGAGACGGCAAGGACAGGGAGAAGTCTCATTGTGGTT
 GAGCACAGGCTGGTTACCATGGTATCGCGGTGGAGTTGTGACCACGTGCATGTCTATG
 GCATGGTCCCCCAACTACTGCAGCCAGCGGCCCGCTCCAGCGCATGCCCTACCAACTAC
 TAGGAGCCAAGGGGCCGGACGAATGTGTCACCTACATCCAGAATGAGCACAGTCGCAAGGG
 CAACCACCACCGCTCATCACCAGAGAAAAGGGTCTTCTCATCGTGGGCCAGCTGTATGGCA
 TCACCTTCTCCCACCCCTGGACC**TAG**GCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
 AGGAGAACGCCTCCGCCAGCCCTAGGCCAGGGACCATCTCTGGCAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCTTGAGGAGGATGTATCTCCAGCCAATCAGGGCC
 TGGGAATCTGTTGGCAATCAGGGATTGGAGTCTATGTGTTAATCAGGGGTGTCTTC
 TTGTCAGTCAGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATTCGAGTCAATCTG
 AGGCTAAGGACATGTCTTCCATGAGGCCTGGTTCAGAGCCCCAGGAATGGACCCCA
 ATCACTCCCCACTCTGCTGGATAATGGGGTCTGTCCCAAGGAGCTGGAACTTGGTGT
 CCCCTCAATTCCAGCACCAAGAACAGAGATTGTGTTGGGGTAGAAGCTGTCTGGAGGCC
 GGCCAGAGAATTGTGGGTTGTGGAGGTTGTGGGGCGGTGGGAGGTCCCAGAGGTGGGA
 GGCTGGCATCCAGGTCTGGCTCTGCCCTGAGACCTGGACAAACCTCTCCCTCTGG
 CACCTCTGCCACACCAGTTCAGTGCAGGAGTCTGAGACCCCTTCCACCTCCCTACAA
 GTGCCCTCGGGTCTGCTCTCCCGTCTGGACCCCTCCAGCCACTATCCCTGCTGGAGGCT
 CAGCTCTTGGGGGTCTGGGTGACCTCCCCACCTCTGGAAAACCTTAGGGTATTTTG
 GCAAACCTCTCAGGGTGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTTTCT
 TAGCCCTCAGCCAGCTGCCATTAGCTTGGCTCTAAAGGGCAGGCCTCTTCTGCCCT
 CTAGCAGGGAGGTTTCCAACTGTTGGAGGCGCTTGGGGCTGCCCTTGTCTGGAGTCA
 CTGGGGCTCCGAGGGTCTCCCTCGACCCCTGTCGTCCTGGATGGCTGTGGAGCTGT
 ATCACCTGGTTCTGCTCCCTGGCTCTGTATCAGGCACTTATTAAAGCTGGCCTCAGTGG
 GGTGTGTTGTCTCCTGCTCTGGAGGCTGGAGGAAAGGGCTTCAGGAGGAGGCTGTGA
 GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGTGATGGGTGG
 GGGCGGTGACTGCCCAACTGGTTGTAATGATTGTACAGGAATAAACACACCTACGC
 TCCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 34

MSSNKEQRSAVFVILFALITILYLSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPII
GNKTLPSRCHQCVIVSSSSHLLGTKLGPETIERAECTIRMNDAPTTGYSAVGNKTTYRVVAH
SSVFRVLRRPQEfvNRTPETVFIFWGPPSKMQPKQGSLVRVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIACHELCDHVHVYGMVPPNYCSQRPRLQRMPYH
YYEPKGDPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

GTTCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACCTCAGCGGACCGGGAGCGACGCAGCTT
 GAGGAAGCATCCCTAGCTGTGGCGAGAGGGCGAGGCTGAAGCCGAGTGGCCGAGGTGTCTGAGGGCTGG
 GGCAAAGGTGAAAGAGTTCAAGAACAGCTCTGGAACCATGACCCATGAAGTCTTGTGACATTATAACCGT
 CTGAGGGTAGCAGCTGAAACTAGAAGAAGTGGAGTGTGCCAGGGACGGCAGTATCTCTTGACCTGGC
 GCCCTATGGGACGTTGGCTCAGACCTTGATACACC**ATG**CTGCGTGGGACGATGACGGCGTGGAGAGGAATG
 AGGCCTGAGGTACACTGGCTGCCCTCCTAGCCACAGCAGGCTGCTTGACTGAAACGAGGCCCTCAG
 GTCACCGTCCAGCCTGCGTCCACCGTCCAGAACGCCGGAGGCAGTGTGATCTGGCTGCGTGGTGAAC
 AGGATGAATGTAACCTGGCGCTGAATGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGCTCATCACC
 CACGGGACCTCGTCATCACTGCCCCAACAAACCAACACTGTGGGAGCGTACCGATGTCGCCCCGGATGCCTGCC
 GGGCTGTGGCCAGCGTGCAGCCACTGTGACACTGCAATCTCAGGACTTCAAGTTAGATGTGCA
 ATTGAAGTGGATGAGGAAACACAGCAGTCAATTGCTGCCACCTGCTGAGAGGCCAACCCAAAGGCCAGGTCCGG
 TACAGCGTCAAACAAGAGTGGCTGGAGGCCAGAGGAACCTGATCATGCCCTCAGGGAACCTCCAGATT
 GTGAATGCCAGGCCAGGAGGACGAGGGCATGTACAAGTGTGCAAGCCTACAAACCCAGTGACCCAGGAAGTGA
 ACCCGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCGCATCATCTACCCCCCAGAGGCC
 CAAACCATCGTCACCAAAGGCCAGAGTCTCATTCTGAGGTGTGTCGCCCCCTGCTGAGGAACTCCACCC
 ACCTGGGCAAGGATGGCTCAGTGTCAACGGCTAACAAAGACGCGCCTCTGCTGAGGCCAACCTCCATCGAC
 ACCAACCGCGAGGAGGACTCAGGCCACCTACCGCTGCACTGGGACAAATGGGTTGGGAGGCCAGGG
 ATCCTCTACAAATGTCAGGTGTTGAACCCCTGAGGTCAACATGGAGCTATCCCAGCTGGTATCCCCTGGGGC
 CAGAGTGCAGCTACCGTGTAGGTGCGTGGGAAACCCCCCGCCCTCCGTGCTGAGGAAATGCTGTGCC
 CTCATCTCCAGCCAGCGCCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGCCTGAGCATGGGCTGAGGAC
 GTCTACCAAGTGCATGGCGAGAACGAGGTGGAGCGCCATGCCGTAGTCCAGCTGCCGACCTCCAGGCCAAC
 ATAACCCCAAGGATGGCAGGATGCTGAGCTGGCTACTGGCACACTCTGTATCACCCCTCAAACCTCGGCAAC
 CCTGAGCAGATGCTGAGGGGCAACCGGGCTCCCGCAGGCTCCCGAGGCTCCATCATCTCAGTGGCCCTGCT
 CCAGGAGAGAAGGGGCAAGGGGCTCCCGCAGGCTCCCGAGGCTCCATCATCTCAGTGGCCCTGAGGAC
 TCATATGAACCTGGTGTGGCGGCTCGGCATGGGAGCTGGCCGGGCCAACCTCTACTATGTGGTAAACAC
 CGCAAGCAGGTACAAATTCTCTGACGATTGGACCATCTCTGGATTCCAGCCAACCCAGCACCGCCTGACCC
 ACCAGACTTGACCCCGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAACCTGTGCGGGAGAGGCCAGACAGCC
 ATGGTCACCTTCCGAACTGGACGGCGCCAAACCCGAGATCATGGCAGCAAAGAGCAGCAGATCCAGAGAGAC
 GACCCCTGGAGGCCAGTCCCGAGACGAGCCAGGCCAGACGCCAGGGCCCTCTCCCCCCCAGAAGCTCCGACAGG
 CCCACCATCTCCACGGCTCCGAGACCTCAGTGTACGTGACCTGGGATCTCCCGTGGGAATGGTGGGTTCCCA
 CAGTCCTTCCGTGTGGAGTACAAGAGCTAAAGAAAGTGGAGACTGGATTCTGGCCACCCAGCGCCATCCCC
 TCGCGGCTGTCGTGGAGATCACGGGCTAGAGAAAGCACCTCTACAAGTTGAGTCGGGCTCTGAAACATG
 CTGGGGAGAGCGAGCCCAGCGCCCCCTCTGGCCCTACGTGGTGTGGGCTACAGCGGTGCGGTGACGAGAGG
 CCCGTGGCAGGTCTTATATCACCTCACGGATGCGGTCAATGAGACCACCATATGCTCAAGTGGATGTACATC
 CCAGCAAGTAACAAACACCCCAATCCATGGCTTATATCTATTATGACCCACAGACAGTGA
 GACAATGATGATAGT
 GACTACAAGAAGGATATGGTGAAGGGGACAAGTACTGGCAGCTTACGCCCCACTGAGCCAGAGAACCTCTAC
 GACATTAAAGATGCACTGCTTCATGAAGGAGGGGAGAGCGAGTTCAGCAACGTGATGATCTGTGAGGAC
 CCGAAGTCTCTGGCCAGCCTGGTCACTGCCACCCCCAACCTCTGGGCTCTGAAACATG
 ATAGAGCGGCCGGTGGGACTGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTCGGGGCTGTC
 CTGGGCTCCATCGTTCTCATCGTCACCTCATCCCCCTCTGCTGTGGAGGGCTGGCTAAGAAAAACAT
 ACAACAGACCTGGTTTCCTCGAAGTGCCCTCCACCCCTGCCGTATACTATGGTGCCATTGGGAGGACTC
 CCAGGCCACCAGGCCAGTGGACAGGCCCTACCTCAGTGGCATGAGGCCCTGTGCTAATGGGATCCACATG
 AATAGGGGCTGCCCTCGCTGAGGGCTACCGGGCATGAAGCCCCAGCAGCAGTGGCCAGGCGAGCTCAG
 CAGCAGAGTGAACACCAGCAGCCTGCTGAGGAGACCCATCTGGCAATGGATATGACCCCCAAAGTC
 ACCAGATC
 ACGAGGGTCCAAGTCTAGCCGGACGAGGGCTTTCTTATACACACTGCCGACGACTCCACTCACCAGCTG
 CTGAGCCCCATCACGACTGCTGCCAACGCCAGGAGCAGCCTGCTGTGGGGCAGTCAGGGGTGAGGAGAGCC
 CCCAGCTCTGGCTGGAAGCAGTGTGGACCCCTCCATTCACTCAGGGCCCCATGCTGCTGGCCTGTC
 CCAGTTGAAGAGGGTGGACAGTCTGACTCTGCCAAGTGAAGTGGAGGAGACTGGTGTCCCCAGC
 ACCTGGCTAGGGACAGGAACCTGGAATGCAGCTCTCCCGGGGCACTGGTGCCTGTGCTTGA
 AAAACACCACCT
 CTCACAATT**TAG**GCAGAAGCTGATATCCCAGAAAGACTATATTTTTTTTTTTTTTTTTTT
 AGAGACAGAGAAATTGGTATTATTTCTATTATAGCATATTATATATTATGCACTTGTAAATAAATGTA
 TATGTTTATAATTCTGGAGAGACATAAGGAGTCCTACCCGTTGAGGTGAGGAGAGGAAATAAAGAGCTGCCA
 CCTAACAGGAGTCACCCAGGAAAGCAGGCCACAGGCTGGCGGGACAGACTCTAACCTGGGCTCTGCA
 GCAGGCGAGGCTGCAGGAGGCCACAGATAAGTGGCAAGAGGAAGGATCCCAGGCACATGGTCA
 TGAGGGAACAGCAAGGGCACGGTATCACAGCCTGGAGACACCCACAGATGGCTGGATCCGGTGCTACGGGAA
 ACATTTCCTAAAGATGCCCATGAGAACAGACCAAGAACAGATGTGACAGCACTATGAGCATT
 AAAACCTCCAGAAT
 CAATAATCCGTGGCAACATATCTGTAAAAACAAACACTGTAACCTCTAAATAATGTTAGTCTCCCTGTAAAA

FIGURE 36

MLRGTMATWRGMRPEVTIACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVLGVVEPP
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHPKAQVRYSVKQEWLEASRGNYLIMPSGNLQ
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRSTAEEAARIIYPPEAQTIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRRLS
 RRALRVLSMGPEDEGVYQCMAENEVGSAAVVQLRTSRPSITPRLWQDAELATGTPVSPSK
 LGNPEQMLRGQPALPRPPTSVGAPSPKCPGEKGQGAPAEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGI PANQHRLTLTRLDPGSLYEVEEMAAYNCAGE
 GQTAMVTFRGRRPKPEIMASKEQQIQRDDPGASPQSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWI PRGNGGFPIQSFRVEYKKLKVGDWILATS AIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEEPSAPS RPYVVSGYSGRVYERPVAGPYITFTDAVNETTIMLKWMYIPASNNNT
 PIHGFYIYYRPTSDNDSDYKKDMVEGDKYWH SISHLQPETSYDIKMQCFNEGGESEFSNVM
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL
 II VTFIPFCLWRAWSKQKHTTDLGFP RSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCPSAAVGYPGMKPQQHCPGELQQQSDTSSLRQTHLGNGYDPQSHQITRGPK
 SSPDEGSFLYTL RDDSTHQLLQPHDCCQRQECPAAVGQSGVRRAPDSPVLEAVWDPPFHSG
 PPCCCLGLVPVEEV DSDP DSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGTCGTATGATCCGGACCCATTGTCGGCCTCTGCCCATCGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCCCGCGAAC**ATG**CAGCCCACGGGCCGCAGGGTTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGCGTCTGCTCCTGCTACTGCTGCTGCTGCTGCCAGC
 CCGTAACCGCGCGAGACCACGCCGGCGCCCCAGAGCCCTCTCACGCTGGGCTCCCCC
 AGCCTCTTCAACCACGCCGGGTGTCCCCAGGCCCTCACTACCCAGGCCTCACTACGCCAGG
 CACCCCCAAACCTGGACCTCGGGTCGCGCGAGGCCCTGATGCGGAGTTCCACTCG
 TGGACGGCCACAATGACCTGCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTCAGCCATGGTCAGACCAGCCCTGGACAGGCTTAGAGACGCCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCTCCTACTCTGAACCTGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCCTATTGGCGTGAGGG
 TGGTCACTCACTGGACAGCAGCCTCTGTGCTGCGAGTTCTATGTGCTGGGGTGCCT
 ACCTGACACTTACCTCACCTGCAGTACACCATGGCAGAGAGTCCACCAAGTTCAGACAC
 CACATGTACACCAACGTCAAGCGGATTGACAAGCTTGGTGAGAAAGTAGTAGAGGGAGTTGAA
 CCGCCTGGCATGATGATAGATTGTCCTATGCATGGACACCTTGATAAGAAGGGCCTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCACTCAGCTGCCAGAGCTGTGTGACAATTG
 TTGAATGTTCCCGATGATATCCTGCAGCTCTGAAGAACGGTGGCATCGTGTGACACT
 GTCCATGGGGTGCTGCAGTGCAACCTGCTGCTAACGTGTCCACTGTGGCAGATCACTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATGGGATTGGTGGAAATTATGACGGACT
 GGCGGTTCCCTCAGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTCAAGGTGTCTCGTGGAAACCTGCTGCCGTCT
 TCAGACAAGTGGAAAAGGTGAGAGAGGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTT
 CCATATGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATGGGTCCCTGGAGGCTCAAATGCCT
 CCCATACCTTGTCCAGGCCTTGTGGCTGCCACCATCCAACCTCACCCAGTGGCTC
 TGCT**TGA**CACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCCT
 AGTCATTACAAGCATATGCTGAGAATAACATGTTACACATGGAAAA

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLRLQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTPGLTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWASAVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLAQCLIGVXGGHSLDSSLSVLRSFYVLGVRYLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLLEVSQAPVIFSHSAARAVCDNLLNPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEEELQGVLRGNLLRVFRQVEKVRREESRAQSPVEAEFPYGQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGCCACAATGCACCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCGGCTTGCTGGCCAGCAAGCCTGATAAGC**ATG**
 AAGCTCTTATCTTGGTGGCTGTGGTGGGTGTTGCTGGTCCCCAGCTGAAGCCAACAA
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGCACA
 TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCAGGCCA
 GTGCCTGGCATGACGTGGAGGCCTACTGCCTGCTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTATCATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
 ACATGGCCTTCCTGATGCTGGTGGACCCCTGTATCCGAAAGCCGGATGCATACTGAGCAA
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGTGGAAAGCTGC
 AGGTGCAGGAGCAGCGGAAGACAGTCTCGATGGCACAAGATGCTCAGC**TAG**ATGGGCTGG
 TGTGGTTGGGTCAAGGCCAACACCATGGCTGCCAGCTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTCCCTCGGTTCCAGTCTCCCTTAAAAGCCTGTGGCATTTCCTCCTT
 CTCCCTAACCTTAGAAATGTTGACTTGGCTATTGATTAGGAAAGAGGGATGTGGTCTCT
 GATCTCTGTTGCTTCTTGGGCTTGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTGAGGCCCTCAGGAGTGGATGCGATCTGTCTCCTGGCTCCACTCTG
 CCGCCTCCAGCTCTGAGTCTGGGAATGTTACCCCTGGAAGATAAGCTGGTCTTCA
 GGAACTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTGAGCATGTGTTCTTCTGCAGTG
 GTTCTTATCACCAACCTCCCTCCCAGCCCCGGCCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCAGTGGCTTCAGGGTGCAGTGGA
 AGCTGGTGGTCTGCTGCCCCCTGCACTTCTCGCACTGGGCATGGAGTGCCATGCATACT
 CTGCTGCCGGTCCCTCACCTGCACTTGAGGGCTGGCAGTCCCTCCTCCCCAGTGTC
 CACAGTCAGTGGCCAGACGGTCGGTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCCCTGTAATTGGGTTGCCTCTTGTCCCTGAACCTCGTTGTACCAAGTGCATGGA
 GAGAAAATTGTCCTTTGTCTTAGAGTTGTGTAAATCAAGGAAGCCATCATTAAATTG
 TTTTATTCCTCTCA

FIGURE 40

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPEANKSSEDIRCKCICPPYRNISGHINYQNVSQKDCNCLHVVEPM
PVPGHDVEAYCLLCECRYERSTTIKVIIVIYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGTCTCGCTTGGGTCCGCTAATTCTGTCTTGAGGCCTGAGACTGAGTCATAGGGTCTGGTCCCCGA
 ACCAGGAAGGGTTGAGGAACACAATCTCAAGCCCCCGCACCAAGTGAGGGGCCCGTGTGGGTCTCCC
 TCCCTTGCATTCCCACCCCTCCTGGCTCTTCTGGGACCCCTCCGGGAGA**TG**CCGGTTGAT
 CGGAGCAAGGATTCTGCTCTGCTGCTCCTACTGGCCGGTGTGATGGTGGAGAGCTCACAGATCGGAGT
 TCGCGGGCAAACACTCAACTCCATCAAGTCCTCTGGGGAGACGCCCTGGTCAGGCCCAATCGATCTGCG
 GGCATGTACCAAGGACTGGCATCGCGCAGTAAGAAGGGCAAAACCTGGGCAGGCCAACCTGTAGCAGT
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGATGGTGTGGAGA
 AAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGTT
 ACTGAAAGCATTAAACCCCTCACATCCCGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC
 TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACACACACTAAGATGTACATATAAAAGGGCATGAAGGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTGCTGTGCTCGTCATTCTGGACAAAATCTGCAA
 CCAGTGCCTCATCAGGGGAAGTCTGTACCAAACAACGCAAGAAGGGTTCTCATGGGCTGAAATTTCAGCGT
 TGCAGACTGTGCGAAGGGCCTGTCTGCAAAGTATGGAAAGATGCCACCTACTCCTCAAAGCCAGACTCCATGTG
 TGTCAGAAAATT**TGA**TCAACATTGAGGAACATCATCAATTGCAAGACTGTGAAGTTGTGTATTAAATGATTATAG
 CATGGTGGAAAATAAGGTCAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAAATATAGATGATCACA
 AAAGGGAGAAAGAAAATGAACACTGAATAGATTAGAATGGGTGACAAATGCAGTCAGCCAGTGTTCATTATG
 CAACTTGTCTATGTAATAATGTACACATTGTTGAAAATGCTATTATAAGAGAACAGCACAGTGGAAATT
 ACTGATGAGTAGCATGTGACTTCCAAGAGTTAGGTTGTGCTGGAGGAGAGGTTCTTCAGATTGCTGATTGC
 TTATACAAATAACCTACATGCCAGATTCTATTCAACGTTAGAGTTAACAAATACTCCTAGAATAACTTGT
 TACAATAGGTTCTAAAAATAAGGCTAACACAGAAATGAAAACATGGAGCATTGTTAACACAGAAAAT
 TACCTTTGATTGTAACACTACTCTGCTGTTCAATCAAGAGTCTGGTAGATAAGAAAAAAATCAGTCATAT
 TTCCAATAATTGCAAATAATGGCAGTTGTTAGGAAGGCCTTTAGGAAGACAAATAACAAACAAACAG
 CCACAAATACTTTTCTAAATTAGTTTACCTGTAATTAAAGAAACTGATAACAGACAAAACAGTCC
 TTCAGATTCTACGGAATGACAGTATATCTCTTATCCTATGTGATTCTGCTCTGAATGCATTATATTTC
 AACTATACCCATAAATTGTAAGTAAATACATGTATTCAACATACACTCTGTGTTAGAGACTTAAGCTGGATCTGACTG
 GATGTCAAATATATGTGGAAAAGAGCTAACAGAGAGATCATTATTCTTAAAGATTGGCATAACCTATATT
 GATAGAATTAGATTGTTAAATACATGTATTCAACATACACTCTGTGTTAGAGACTTAAGCTGGATCTGACTG
 CACTGGAGTAAGCAAGAAAATTGGGAAAATTTCGTTGTTAGGTTGGCAACACATAGATCATATGTCTG
 AGGCACAAGTGGCTGTTCATTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTGCTAT
 CATAATATTACTATGCAGATGAATTCACTGAGTGTGAGGTCTGTGCTCGTACTATCCTCAAATTATTATTT
 TGCTGAGATCCTCAAATAATCTCAATTTCAGGAGGTTCACAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG
 TTTCATTGCCCTCTATAAGCTCTGACTAGCCAATGGCATCATCCAATTCTCCAAACCTCTGCAGCATCTG
 CTTTATTGCCAAAGGGCTAGTTCGGTTCTGCAGCCATTGGTTAAAAAAATAAGTAGGATAACTTGTAAA
 ACCTGCATATTGCTAATCTATAGACACCACAGTTCTAAATTCTTGAACCACTTACTACTTTTTAAACTT
 AACCTCAGTTCTAAATACTTTGTCGGAGCACAAAACAATAAAAGGTTATCTTATAGTCGTGACTTTAAACTTTG
 TAGACCACAATTCACTTTAGTTCTTTACTTAAATCCATCTGCACTCTCAAATTAAAGTTCTCCAGTAG
 AGATTGAGTTGAGCCTGTATATCTTAAATTCACACTTCCACATATAATTACTAAGATGATTAAGACTTA
 CATTCTGCACAGGTCTGCAAAACAAAATATAAAACTAGTCCATCCAAGAACCAAGTTGTATAAACAGGT
 TGCTATAAGCTGTGAAATGGAACATTCAATCAAACATTCTTATATAACAAATTATTATTTACAAT
 TTGGTTCTGCAATTCTTATGTCCACCCCTTTAAAAATTATTGTAAGTAATTATTACAGGAAATG
 TTAATGAGATGTATTCTTATAGAGATATTCTTACAGAAAGCTTGTAGCAGAATATTTGCAGCTATTGAC
 TTGTAATTAGAAAAATGTATAAAAGATAAAACTTAAATTCTCCTCTAAAAACTGAAAAAA
 AAAA

FIGURE 42

MAALMRSKDSSCCLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQGSSACMVCRKKKRCHRDGMCCPSTRCNN
GICIPVTEISILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCRLRS
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

FIGURE 43

TCTCAATCTGCTGACCTCGT GATCCGCCTGACCTTGT AATCCACCTACCTGGCCTCCAAA
 GTGTTGGGATTACAGGC GTGAGCCACCGGCCGGCAACATCACGTTTAAAAATTGATT
 TCTTCAAATT CATGGCAAATATTC C CTTAAC TCTTATGTCAGAATGAGGAAGGA
 TAGCTGCATTATTTAGTCAGTTTCATTGCATAGTAATATTCATGTAGTATTTCTAAG
 TTATATTTAGTAATT CATATGTTAGATTAGGTTAACATACTTGAAAGAAACTTG
ATGT GTTTAAAGCCTGGCAGAAATTCTGTATTGTTGAGGATTGTTCTTTATCCCCCT
 TTTAAAGTCATCCGTCCTGGCTCAGGATTGGAGAGCTGCACCACCAAAATGGCAAACA
 TCACCAGCTCCCAGATTTGGACCAGTTGAAAGCTCCGAGTTGGGCCAGTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACTACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTGACTCAAATCTCAACCTGAGCCATCCC
 CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTGTCTCCT
 CCTGGTTGGAGTCCTTCCCTCCAGGCAAAACTCGAGAATCAACACCTGGAGACAGTCC
 CTCCACTGTGAACAAGCTTTGCAGCTCCAGCAGCACCATTGAAAATATCTGTGTCTG
 TCCACCAGCCACAGCCAAACACATCAAACCTGCTAAGCGGCGGATACCCCCAGCTCTAAG
 ATCCCAGCTCTGCAGTGGAAATGCCGGTCAGCAGATGTCACAGGATTAAATGTGCAGTT
 TGGGGCTCTGGAATTGGGT CAGAACCTCTCTCTGAATTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTCCCATCAGCTGTATTGAGCTTAAAGTGAGCCTTGAATACA
 TCTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGT CATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTCCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTCATCAGAGTCAGCTCCA
 GGAACCATCATGAATGGACATGGGGTGGTCGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTGT CATGGCTGGGCCAACAAACAGAGGAAGAGGAGTAGCTACGTGA
 TGTGGAAAACACCAGTTGGTCAATGGCTCATTCTG **TAAA** AAGCAGCCCTTTGCTTTTGT
 TTTGGACCAGGTGTGGCTGTGGTATTAGAAATGTCTTAACCACAGCAAGAAGGGAGGT
 GGTGGTCTCATATTCTCTGCCCTAATCAGACTGCACCACAGTCAGCAGCATACAGTATGCAT
 TTTAAAGATGCTGGGCCAGGCAGGGTGGCTGATGCCATAATCCAGTGCTTGGGGGCC
 AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTGAGACCACCCCTGGCAACATGGTAAACTC
 TGTCTCTACTAAAATACGAAAAACTAGCCGGGTGTGGTGGCGCGTGCCTGTAATCCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGCTACAAAGTGAGACTCC
 GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQPQPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTSVITSCSLTSSLNSASPVAMSSSYDQSSVHNRIPYQSPVSSSESAP
GTIMNGHGGGRSQQTLD SKYSSKLLL SWLVPTKQRKRIA HVMWKT PVGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGCTGGCGGGGCC **ATG** GCGCTGCCATCCGAATCCTGCT
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGCTGTACACCTGCAACCTGCACCACACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGCACCCGCGCTTCTGACCTGCGTAACCGCGGGCACGTGT
 GGACCGACCGCACGTGGAGGAGGCTAACAGGTGGTGCACGGGACCGGCAGCCGCCGGG
 GTCCCGCACGACCGCGCGACCGCCTGCTGGACCTCTACGCGTCGGCGAGCGCCGCGCTA
 CGGGCCCCTTTCTGCGCGACCGCGTGGCTGTCGGCGGATGCCCTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCCACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCACCTGACGGTCGCCAACCCACGC
 GGAGCCGCCCGGGCTCTCCGGCAACGGCTCCAGCCACAGCGGCCAGGCCCAG
 ACCCCACACTGGCGCGGCCACAACGTATCAATGTATCGTCCCCGAGAGCCGAGCCCAC
 TTCTTCAGCAGCTGGCTACGTGCTGCCACGCTGCTGCTTCACTGCTACTGGTCAC
 TGTCCCTGGCCGCCCGCAGGCGCCGAGGCTACGAATACTCGGACCAGAAGTCGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTGCTGCTGGCTGAGGGGACAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCCTGCCAAGTACATCGACCTAGACAAAGGGTCCGGAAGGAGAACT
GAAA **TAG** GGAGGCCCTGGCTCCTGGCTGGGCTGGCTGACCTCTCCTGTCTGTGCTC
 CTCGGGCATCTCCTGATGCTCCGGGCTCACCCCCCTCCAGCGGCTGGTCCCCTTCC
 GGAATTGGCCTGGCGTATGCAGAGGCCCTCCACACCCCTCCCCAGGGCTTGGTGG
 AGCATAGCCCCACCCCTGCCCTTGTCTCACGGGTGCCCTGCCACCCCTGGCACACC
 AAAATCCCACGTGATGCCCATCATGCCCTCAGACCCCTCTGGCTCTGCCGCTGGGGCCTG
 AAGACATTCTGGAGGACACTCCCACAGAACCTGGCAGCCCCAAAATGGGTGAGCCTCA
 GGGCAGGAGTCCCACCTCCAGGGCTCTGCTCGTCCGGGCTGGGAGATGTTCTGGAGGA
 GGACACTCCCACAGAACTTGGCAGCCTGAAGTTGGGGTCAGCCTCGCAGGAGTCCCAC
 CCTCCTGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCAACCAGTGGACTCCAG
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTGAATGCCAGCCCTGCTCCTGTGTTG
 CTTGGGCCACCTGGGGCTGCACCCCTGCCCTTCTGCCCATCCCTACCCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGCTCCCTGTGACTTCTGACCCCTGACACCCCTCC
 GGACTCTGCCCTGGGCTGGAGTCTAGGGCTGGGCTACATTGGCTTGTACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTTGGTTGGGTGCCCTGTGTTGCCACTCTCAGCACCCACATT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAGCTCCCACATTGATTTAAAAAA
 AAAAA

FIGURE 46

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLA VARGAPALLTCVNRGHVWTDRHVEEAQQVVHWRQPPGVPHDRADRLLDL
YASGERRAYGPLFLRDRVAVGADA FERGDFSLRIEPL EVADEGTYSCHLHHHYCGLHERRVF
HLTVAE PHEA EPPRGSPGNSSHSGAPGP DPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTLAARRRRGGYEYSDQKSGKSKGDVNLA EFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDLDKGFRKENCK
```

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGCGCGTGGCGCAGCGCGAC **ATG** GCC GTGTCTCAGAGGACGACTTT
 CAGCACAGTCAAACCTCACGGAACACAAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
 ACTGCTTGAGAAGCTGCTGGACCGCCCCCTGGCTGCAGAGGCCGAGGACCGCTTCT
 GTGGCACATACATCATCTTCTTCAGCCTGGCATTGGCAGTCTACTGCCATGGAACCTCTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCGCAACTCCTCCAGCCCAGCCACCAGGG
 GGACCCCTGAGGGCTCAGACATCCTGAACTAACCTTGAGAGCTACCTTGCCGTTGCCTCCACCG
 TGCCCTCCATGCTGCTGGTGGCCAACCTCCTGCTTGTCAACAGGGTTGCAGTCCACATC
 CGTGTCTGGCCTCACTGACGGTCATCCTGGCATCTTCATGGTGATAACTGCACTGGTGAA
 GGTGGACACTTCCTCCTGGACCCGTGGTTTTTGCGGTACCATGGTCTGCATGGTGATCC
 TCAGCGGTGCCTCCACTGTCTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTCCTATG
 AGGAACCTCCAAGCAGTGTATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTCCTGACGG
 CCACCATCTCCTCGTGCATGGACTCTACCTGCTGCTCCAGGCTGGAGTATGCC
 AGGTACTACATGAGGCCTGTTCTGCGGCCATGTGTTCTGGTGAAGAGGAGCTTCCCCA
 GGACTCCCTCAGTGCCCTCGGTGGCCTCCAGATTGATTCCCACACACCCCCCTCTCC
 GCCCCATCCTGAAGAAGACGCCAGCCTGGCTCTGTGTACCTACGTCTTCTCATCACC
 AGCCTCATCTACCCGCCGTCACCAACATCGAGTCCTCAACAAGGGCTGGGCTCACT
 GTGGACCACCAAGTTTCATCCCCCTCACTACCTCCTCTGTACAACATTGCTGACCTAT
 GTGGCCGGCAGCTCACCGCCTGGATCAGGTGCCAGGGCCAACAGCAAGGCCTCCAGGG
 TTCTGCTCCTCGGACCTGCCTCATCCCCCTCTCGTGTCTGTAACTACAGCCCCGCGT
 CCACCTGAAGACTGTGGTCTCCAGTCCGATGTGTACCCGCACTCCTCAGCTCCGCTGG
 GGCTCAGCAACGGCTACCTCAGCACCTGGCCCTCCTACGGGCTTAAGATTGTGCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTATGTCTTTATGTGTGCTGGCTTAACACTGGG
 CTCAGCCTGCTCTACCCCTGGTGACCTCAT**TAG**AAGGGAGGACACAAGGACATTGGTG
 CTTCAGAGCCTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCATGGAGGAAAGGCC
 TAAAGTTCACTTGGGACAGAGAGCAGACACTCGGGCTCATCCCTCCAAAGATGCCA
 GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATAATTCCAGTCATATTAAAGAACACT
 CCTGAGACAGTTGAAGAAGAAATGACAAATCAGGGTACTCCCTCACAGCTGATGGTTA
 ACATTCCACCTTCTTAGCCCTCAAAGATGCTGCCAGTGTGCTGGCTTAGAGTTATTACA
 AAGCCAGTGCCAAAACCCAGCCATGGCTTTGCAACCTCCAGCTGCGCTATTCCAGCT
 GACAGCGAGATGCAAGCAAATGCTCAGCTCCTTACCTGAAGGGGTCTCCCTGGAATGGA
 AGTCCCCTGGCATGGTCAGTCTCAGGCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
 GCAGGGTGAACAACTGCCCACTAACCAAGACTGGAAAACCCAGAAAGATGGGCTTCCATGAAT
 GCTTCATTCCAGAGGGACCAGAGGCCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
 TTTCAAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGCAAGATGAGGGTC
 TTTCAGTGTTCCTGTTACAACATGTCAGGCCATTGGTTCAAGGGCGTAATAACTTGC
 GTATTCAAAA

FIGURE 48

MAVVSEDDFQHSSNSTYGTTSSSLRADQEALLEKLLDRPPPGLQRPEDRFCGTYIIFSLGI
GSLLPWNFFITAKEYWMFKLRNSSLATGEDPEGSDILNYFESYLAVALVPSMLCLVANFL
LVNRVAHVIRVLASLTVALAIFMVALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY
LLLSRLEYARYYMRPVLAHVFSGEELPQDSLSAPSVASRFIDSHTPPLRPILKKTASLG
CVTYVFFITSLIYPAVCTNIESLNKGSGSLWTTKFFIPLTFLLYNFADLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSLLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTACCAAGAGCTGGAGACACCA
 TCTCCCACCGAGAGTC**ATG**GCCCATGGCCCTGCACCTCCTGTCCTGTCCTGCCCCATCCTCC
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTGAGAAATGC
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTACCTGGGGCTCAATCGGACCCT
 GAAGCCCCAGAGGGTATTGTGGTGGCGCTGGTGTGGCCGGGCTGGTGGCCCAAGGTGC
 TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATCGGGGCCGCATC
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGAGCTGGGAGCCATGCGATGCCAG
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGGCTAACCTGACCAAGTTCACCC
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTCGCAACTATGTGGTGGAG
 AAGGTGCCGAGAACAGCTGGCTACGCCCTGCCTCCCAGGAAAAGGCCACTGCCCGAAGA
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTAACGGCACTGGGCTGCAGAAAGG
 CGATGAAGAAGTTGAAAGGCACACGCTTGAATATCTTCTGGGGAGGGAACCTGAGC
 CGGCCGGCCGTGCAGCTCTGGAGACGTATGTCCGAGGATGGCTTCTTATCTAGCTT
 CGCCGAGGCCCTCCGGGCCACAGCTGCCCTAGCGACAGACTCCAGTACAGCCGCATCGTGG
 GTGGCTGGACCTGCTGCCCGCGCTGCTGAGCTCGCTGTCCGGCTTGTGCTGTTGAAC
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCACGTGGTGTGCTGACGGCGAGCGGACCGG
 CGGTGAAGCGCATCACCTCTGCCGCCGCTGCCCGCACATGCAGGAGGCCTGGGAGG
 CTGCACTACGTGCCGCCACCAAGGTGTTCTAACGCTTCCGAGGCCCTCTGGCGCGAGGA
 GCACATTGAAGGCCACTCAAACACCGATGCCCGCGCATGATTTCTACCCGCCGC
 CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTGGACGCCGGCAGCGTTCGCC
 GGCTTGAGCCGGGAAGAGGCCTTGCCTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC
 TGTCGTGCCAGCTCTGGACGGCACCGCGCTGCTAACGCTGGCGAGGACCAAGCACA
 GCCAGGGTGGCTTGTGGTACAGCCGCCGGCGCTGGCAAACCGAAAAGGATGACTGGACG
 GTCCCTATGGCCGCATCTACTTGCCTGGCGAGCACACGCCAACCGCCTACCCGCACGGCTGGTGG
 GACGGCGGTCAAGTCGGCGCTGCCGCCATCAAGATCAACAGCCGAAGGGGCCATGCAT
 CGGACACGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGCAGGGCATGTGCATGGG
 GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCCTCAGTCCAAGG
 CCAGTTATCTCTCCAAAACACGACCCACACGAGGACCTCGCAT**TAA**AGTATTTGGAAAAAA
 AAA

FIGURE 50

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSAGHKVTILEADNRIGGIFTYRDQNTGWIGELGAMRMPSSHRIIL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKPEKLGYALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGLNSRPAVQLLGDMSEDGFYLSFAEALR
AHSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHQIETSPARNL
KVLKADVVLITASGPRAVKRITFSPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCTGACTCGGGACAGCTCAGAGCAGGGCAGAAGTGGGACACTCTGGCCGGCCTCTGCCTGC**AT**
GACGCTCTGAAGCCACCTGTCTGGAGGAACCACGAGCAGGGAAAGAAGGACAGGGACTCGTGTGGCAGGAA
 GAACTCAGACGGGAAGCCCCCATCACTAGAACGACTGAGAGATGCCGCCCCCTCGCAGGGCTGAATTTCCT
 GCTGCTGTTACAAAGATGCTTTATCTTAACCTTTGTTCCCCACTTCGACCCGGCGTTGATCTGCAT
 CCTGACATTGGAGCTGCCATCTTCTGTGGCTGATCACAGACCTCAACCCGCTTACCTCTTGACCTGAA
 CAATCAGTCTGAGGAAATTGAGGGAGGAGCACCGAAGGGGTTTCCCAGAAGAACAAATGACCTAACAGTTGCTG
 CTTCTCAGATGCCAACAGACTATGTATGAGGTTCCAAGAGGACTCGCTGTGCTGACAATGGGCCCTGCTGG
 ATATAGAAAACCAACCAGCCATCACAGATGGCTATCTTACAAACAGGTGCTGATAGAGCAGAGTACCTGGGTC
 CTGCTCTTGATAAAAGTTATAAATCATCACCAGACAGCTTGTGCGCATCTTGCTCAGAATAGGCCAGAGTG
 GATCATCTCGAATTGGCTGTTACAGTACTCTATGGTAGCTGTACCTCTGTATGACACCTGGGACCAGAAC
 CATCGTACATATTGTCAACAAGGCTGATATGCCATGGTGTACTGTGACACACCCAAAAGGCATTGGTGTGAT
 AGGAAATGTAGAGAAAGGCTCACCCGAGCCTGAAGGTGATCATCTTATGGACCCCTTGATGATGACCTGAA
 GCAAAGAGGGAGAAGAGTGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTTCAG
 AAAACCTGTGCCCTCTAGCCCAGAACGACCTGAGCGTACCTGCTCACCAGTGGGACCACAGGTGACCCAAAGG
 AGCCATGATAACCCATCAAATATTGTTCAAATGCTGTCCTTCTCAAATGTGTGGAGCATGCTTATGAGCC
 CACTCCTGATGATGTGGCATATCCTACCTCCCTGGCTCATATGTTGAGAGGATTGTACAGGCTGTTGTGTA
 CAGCTGTGGAGCCAGAGTTGGATTCTCCAAGGGGATATTGGTGTGGCTGACGACATGAAGACTTGAAGCC
 CACATTGTTCCCGCGGTGCGCTCGACTCCTAACAGGATCTACGATAAGGTACAAATGAGGCCAACACCCCT
 GAAGAAGTTCTGTTGAAGCTGGCTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATA
 TTTCTGGGACAAGCTCATCTTGCAAAGATCAGGACAGCCTGGCGGAAGGGTCTGTGTAATTGTCAGTGGAC
 TGCCCCCATGTCACCTCAGTCATGACATTCTCCGGCAGCAATGGGATGTCAGGTGATGAAAGCTTATGGTCA
 AACAGAATGCAACAGGTGGCTGTACATTACATTCTGGGACTGGACATCAGGTACAGTGGGGTGCCTGGC
 TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACACTTACAGTGAATAATGAAGGAGAGGTCTGCAT
 CAAGGGTACAAACGTCTCAAAGGATACCTGAAAGGACCCCTGAGAACAGCACAGGAAGGCCCTGGACAGTGT
 GCTCACACAGGAGACATTGGCGTGGCTCCCGAATGGAACACTCTGAAGATCATCGACCGTAAAAAGAACATT
 CAAGCTGGCCAAGGAGAACATATTGCAACAGAGAACGATAGAAAATCTACAAACAGGAGTCAACCAGTGT
 AAATTGTCACAGGGAGAGCTTACGGTCATCCTTAGTGGAGTGGTGTCTGACACAGATGTACTTCCCTC
 ATTGTCAGCCAAGCTTGGGTGAAGGGCTCCTTGAGGAACGTGACAAACAGTTGTAAGGGAGCCATT
 AGAAGACTTGCAAGAAATTGGGAAAGAAAGTGGCTTAAACACTTTGAACAGGTCAAAGCATTTCATCC
 AGAGCCATTTCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTCAAATACT
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGCCACTG
 TGCAGCTGTGAGAAAATGGATTAAAATCTTACATTGTTGCTTCTCTCTTACATTGTTTAAACATGCTTCA
 TGTAAACTCTAAAGCCATAGCTTGTATATTGAGACATATAATGTGTAACACTTGTGCTTCTCTTAAACAT
 ATCTGTCTTCCATCTCGATGTTGCTAATATTAAAGGCTCAGGGCTACTTTATCAACATGCTGTCTCAA
 GATCCCAGTTATGTTCTGTGCTCTCCTCATGATTCCAACCTTAACACTATTAGTAACCAAGTCAAGGGT
 CAAAGGGACCCCTGTGCCCTCTTGTGATAAAACATAACTGCCAACAGTCTATGCTTATTACA
 TCTCTACTGTTCAAACAAAGAGATTAAATTCTGAAAAGCTGCTTACAATTGTTCTAGCCACTCCAC
 AAACCAACTAAATTAGTTAGCCTATCACTCATGTCATCATATCTATGAGACAAATGTCTCCGATGCTCTT
 CTGCGTAAATTAAATTGTTGACTGAGGGAAAAGTTGATCATACCAACATTCTCTAAACTCTTAGTTAGATA
 TCTGACTTGGGAGTATTAAGGCTATGACATACTGCTCCAAAAGGAATGCTGTTCTAAAGCATTATT
 CAGTAGGAACCTGGGAGTAAATCTGTTCCCTACAGTTGCTGAGCTGGAAGCTGTGGGGAGGGAGTTGACA
 GGTGGGCCAGTGAACCTTCCAGTAAATGAAGCAAGCAACTGAATAAAAACCTCTGAACGGAAACAAAGATCT
 ACAGGCAAGCAAGATGCCACACAAACAGGCTTATTTCTGTGAAGGAACCAACTGATCTCCCCACCTTGGATT
 AGAGTTCTGCTTACCTTACCCACAGATAACACATGTTGTTCTACTTGTAAAGTCTTAAAGTCTTAAAC
 TATTACAGATAAAAAAA

FIGURE 52

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CCFSDAKTMYEVQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPWEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSSLKVIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSAAAFLKCVEHAYEPTPDDVAISYLPALAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFKELOKGIIRHDSFWDKLIFAKIQDSLGGRVRVIVTGAAPMSTSVMFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHGVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPKTQEALDSDGWLHTGDIGRWPNGTLKIIDRKKNIFKLAQGEYIAPEKIEINIYNR
SQPVLQIFVHGESLRSSLGVVVVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSIENGLLPTLAKRGELSKYFRTQIDSPLYEHIQD
```

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGC GGAGGCCGCGCGAGCCGGCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG
 CCCGGGCCCTAAGCATTCTGAAGTCATGGCTGCCAGGACATTGGTGAACCGCCAAT
 CCGGT**ATG**ACGACTGGAAGCCCAGCCCCCATCAAGCCTTGGGCTCGGAAGAACGG
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGCCCTGCCAGGAGATTCTGTCA
 GACAGGGCCGTGCTTCTGCTGGTACTGTCATTGCAATATCAAGTTGATCCTGGACA
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC
 CTAGGCCGCTGGAGCCCCACGGCGAGAGCAGTGGTCCCCGGCGGGTCCTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCA CGGTGCTGGAGGATG
 AGGCCGGGAGCAGGGCCGGGCATCCATGTCATTGCTCTCAACCAGGCCACGGCACGTG
 ATGGCAAAACGTGTGTTGACACGTACTCACCATGAGGATGAGGCCATGGTGTATTCT
 CAACATGGTAGCGCCCGGCCAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTCCACC
 TCAAGGACACAGCCAAGGCTGCTGAGGAGCCTGGCAGCCAGGCTGCCCTGCCCTGGGC
 TGGAGGGACACATGGCCCTCGTGGACGAAAAGGAGGTCTGTCTCGGGGAGAAACATT
 TAAGTCACCTGCCCTCTTCCCTGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGCAGACACAGAGCTGAACCGTCGCCGGCGC
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAAGGACCCCACACCATCGA
 GTTCAGCCCTGACCAACTCCCAGACAACAAGGTCTCAATGTGCCTGTGGCTGTCATTGCA
 GGAACCGACCCAATTACCTGTACAGGATGCTGCGCTCTGCTTCAAGCCAGGGGTGTCT
 CCTCAGATGATAACAGTTTCAATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT
 GTTGGTCTGAGGGCATCCAGCATCTCCATCAGCATCAAGAATGCCCGTGTCTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTCAACCTGTTCCGGAGGCCAAGTTGCTGTGGTT
 CTGGAAGAGGACCTGGACATTGCTGTTGATTTTCAGTTCTGAGCCAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTGCCTGGAATGACCAGGGTATGAACACA
 CGGCTGAGGACCCAGCACTGTACCGTGTGGAGACCATGCCCTGGCTGGCTGGGTGCTC
 AGGAGGTCTGTACAAGGAGGAGCTTGAGCCAAGTGGCTACACCGGAAAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCCATCAACACGCCGGGGCAGAGTGCACTCATCCCTGACG
 TTTCCGATCCTACCACTTGGCATCGTCGCCCTCAACATGAATGGCTACTTCAAGGAGGCC
 TACTCAAGAAGCACAAGTTCAACACGGTTCCAGGTGCTCAGTCAAGGAGGCTGAGGTTCTGGACC
 GAAGAAAGAAGCTTATGAAGTGGAAAGTTCACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
 ACAGCAAGAACCCCTGTGAAGACTCTTCCCTGCCAGACACAGAGGGCCACACCTACGTGGCC
 TTTATTGAATGGAGAAAGATGATGACTTCACCACTGGACCCAGCTGCCAAGTGCCTCCA
 TATCTGGGACCTGGATGTGCGTGGCAACCATGGGGCTGTGGAGATTGTTCGGAAGAAGA
 ACCACTCCCTGGTGGTGGGGTCCCGCTTCCCTACTCAGTGAAGAACGCCACCCCTCAGTC
 ACCCCAAATTCCCTGGAGCCACCCCAAAGGAGGAGGGAGGCCAGGAGCCCAGAACAGAC
ATGAACCTCCCTCCAGGACCCCTGCCGGCTGGTACTGTGTACCCCCAGGCTGGCTAGCCCT
 TCCCTCCATCCTGTAGGATTTGTAGATGCTGGTAGGGCTGGCTACCTTGTGTTTAACA
 TGAGACTTAATTACTCAAGGGGAGGGTCCCTGCTCCAACACCCGTTCTGAGTT
 AAAAGTCTATTATTACTTCCCTGTTGGAGAAGGGCAGGAGAGTACCTGGAAATCATTACG
 ATCCCTAGCAGCTCATCCTGCCCTTGAATACCCCACTTCCAGGCCTGGCTCAGAACATCTA
 ACCTATTATTGACTGTGCTGAGGGCCTGAAAACAGGCCGAACCTGGAGGGCTGGATTTC
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGCTGGCTTACTCAGGAAACTGCTGTGCC
 CAACCCATGGACAGGCCAGCTGGGCCACATGCTGACACAGACTCACTCAGAGACCCTA
 GACACTGGACCAGGCCCTCTCAGCCTTCTTGTCCAGATTCCAAAGCTGGATAAGTT
 GGTCAATTGATTAAGGAGAAGCCCTCTGGAAAAA

FIGURE 54

```
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><subunit 1 of 1, 660 aa, 1 stop
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RAISEANEDPEPEQDYDEALGRLEPPRRGSGPDRVLDVEVYSSRSKVYVAVDGTTVLEDEA
REQGRGIHVIVLNQATGHVMAKRVFDTYSPEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRRLRFCSKVEGYGSVCSCDKPTPIEFSPDPLPDNKVVLNPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVFIDGYEPMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPKEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNDSLKEAYEVHRLLSEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVRGNHRGLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
```

Important features of the protein:

Transmembrane domain:

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGCTGGTGGAAAGGCCTAAGAACGAACTGGAAAGCCCCTCTCTTGAACCACAC
 CTGTTAAAGAACCTAACGACCAATTAAAGCCACTGGAAATTGTTCTAGTGGTTGGGTGAATA
 AAGGAGGGCAGA**ATGG**GATTCATCTCATTAGGCCGCTGTCTGGCTATGGTGGGGATGTTA
 CGTGGCCGGAATCATTCCCTGGCTGTTAATTCTCAGAGGAACGACTGAAGCTGGTACTGTTGG
 GTGCTGGCCTCTGTGGAACTGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTATGAA
 GATATTCTGAGGGAAAACACCACCAAGCAAGTGAACACACATAATGTGATTGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCATGAACATGAGCACAGCCACGACCACACAGCTGCATGCCTATATTGGTG
 TTTCCCTCGTTCTGGGCTCGTTCATGTTGCTGGTGGACAGATTGTAACCTCCATGTGCATTCT
 ACTGACGATCCAGAACAGCAGCAAGGTCTAGCAATTCAAATCACCACACGCTGGGTCTGGTTGTCCA
 TGCTGCAGCTGATGGTGGCTTGGGAGCAGCAGCATCTACTCACAGACAGCTGTCAGTTAATTG
 TGTTTGTGGAATCATGCTACATAAGGCACCAGCTGCTTTGGACTGGTTCTTGCATTGGCAGCACAGTTATGTCCAT
 GGCTTAGAGCGGAATCGAACAGAAAGCACTTGCTGGTCTTGCACTGGCAGCACAGTTATGTCCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAACGCCCTTCAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTCTCTGCCGGACATTCTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGCGGA
 ATAGGGCACAGCCACAAGCCCGATGCCACGGGAGGGAGAGGCCTCAGCCGCCTGGAAGTGGCAGCCCT
 GGTTCTGGGTGCCTCATCCCTCATCCTGTCAGTAGGACACCAGCAT**TAA**ATGTTCAAGGTCCAGC
 CTTGGTCCAGGGCCGTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTCCTCAGTC
 TCTGTCTCACCTGCGCATCTACATGTATTCTAGAGTCAGAGGGGAGGTGAGGTTAAAACCTG
 AGTAATGGAAAAGCTTTAGAGTAGAACACATTACGTTGAGTTAGCTATAGACATCCCATTGTGT
 TATCTTTAAAAGGCCCTTGACATTTCGCTTTAATATTCTCTTAACCCATTCTCAGGAAAGATG
 GAATTAGTTAAGGAAAAGAGGAGAACCTCATACTCACAATGAAATAGTGATTATGAAAATACAGT
 GTTCTGTAATTAAGCTATGTCCTTCTTAGTTAGAGGCTCTGCTACTTTATCCATTGATTTT
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 ACCTGTCTCCACATTCTAGAGAGGAGCCAAGTTCTAGTAGTTCTAGGCTTCTCAAGAA
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 GGCAACTGTGCTCTCACATAACCACCTGAGCAAGATGGATCATAAAATGAGAAGTGTGCTA
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 TCCCTCTAGCCTCTCCCTGCCACAATTGCTGCTACTGCTGGTGTAAATATTGTGTTGGATGAATT
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 GACTGGTGTGAGACTTGAGGTTCATCTAGTCCTCAAAACTATATGGTGCCTAGATTCTCTGGA
 AAC TGACTTGTCAAATAGCAGATTGTAAGTGTCAAAAAAA

FIGURE 56

MDDFISISISSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVVDQ
IGNSHVHSTDDPEAARSSNSKITTLGLVVHAAADGVALGAAASTSQTSQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLIILSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGGCGGCAGGGAGAGCGACCCGGCGGCCTCGTAGCAGGGGCCCCGGATCCC
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTGAG**ATG**ATGGGCTTGG
 GAAACGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCAGGCCCTGGTGGCCTGCATC
 ATCGTCTTGGCTTCAACTACTGGATTGCGAGCTCCCGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
 AGAACGAGTTCCAGGGAGAGCTGGAGAACAGCAGCGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTGGTGA
 TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCCTCAGTTCAAAGAACAGACCAACCTGGAG
 AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTCCAGAGACCTGA
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCCCTGCCACACACAGAGGTGCCACAAGGGAAACGTGCTGGTAACAGCAA
 GTCCCAGACACCAGCCCCCAGTCCGAAGTGGTTGGATTCAAAGAGACAAAGTTGAGAAAG
 AGGAAACCAATGAGATCCAGGTGGTAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
 CCAGGCCGGAGCAGGTGGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGAGCCGG
 AGAACTGGGCCAGACCCCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA
 TGGAGGGCCCTGAGCGAGACCAGCTTGTATCCCCGACGGACAGGAGGAGCAGGAAGCT
 GCCGGGAAGGGAGAAACCAGCAGAAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
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 TTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTACTTGATCAGCGTGAAGCGGG
 AATCATAACACTC**TGA**ATTGAACTGGAATCACATATTCACAACAGGGCGAAGAGATGACTA
 TAAAATGTTCATGAGGGACTGAATACTGAAAATGTACTAAATAATGTACATCTGA

FIGURE 58

MMGLGNRGRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTEGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDQRQQLQALSEPQPRLQAAGLPHTEVPGKGNVLGNSKSQTPAPSSEVVLDSKR
QVEKEETNEIQVVNEEPQRDRLPQEKGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQKLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRTDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

FIGURE 59

GG**ATG**CAGAAAGCCTCAGTGTGCTCTTCCTGGCCTGGGCTGCTTCCCTTCTACGCTGGCATTGCCCTTTCA
 CCAGTGGCTTCTGCTCACCCGTTGGAGCTCACCAACCATAAGCAGCTGCCAAGAGCCCCCAGGCCCTGGTCCC
 TGCATGGGGAGCCAAGGGAAACCTGGGCCCTGGATGGCTTCCGAGTTTCGCGGGTTGTGGTGTGA
 TAGATGCTCTGCGATTGACTTCGCCAGCCCCAGCATTACACGCTAGAGAGCCTCTGTCTCCCTACCCCT
 TCCTGGCAAACTAAGCTCCTTGCAAGAGGATCCTGGAGATTAGCAGCCCCACCATGCCGCTAACGATCTCAGG
 TTGACCCCTCCTACCACCACATGCAGCCTCAAGGCCCTCACCACGGCTACTGCCTACCTTATTGATGCTG
 GTAGTAACCTGCCAGCACGCCATAGTGGAAAGACAATCTCATTAAGCAGCTACCCAGTCAGGAAGGGTAG
 TCTCATGGGAGATGATACTGGAAAGACCTTTCCCTGGTGTCTTCTCAAAGCTTCTTCCCATCCTCA
 ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCTACCCCACCATGGACAGTGGTAATGGG
 ACGTGTGATTGCTCACTCCTGGGTGTGGACCTGTGGCCACAAGCAGTGGCCTCACCACCCGAAATGGCCA
 AGAAACTTAGCCAGATGGACCAGGTGATCCAGGGACTGTGGAGGCTGGAGAATGACACACTGCTGGTAGTGG
 CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGACAGTGAGCTGGAGGTCTAGCTGCTCTTT
 TGTATAGCCCCACAGCAGTCTCCCCAGCACCCACCAAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTGTGC
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 GGGTGAGGACTCCCAGCCCCACTCCTCTGCTTAGGCCAACGCTCAGCTCTCATCTCAATGTCAGCAGGTGT
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 TCTCCAAGGCCCTGCTGACTACCAGTGGCTCTCCAGAGCCCCAAGGGGGCTGAGGCACACTGCCACTGTGA
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 GCATGGCGGGGGTACTGCTCTTGGCTGCTTATCTGCTGCTGCATCTCAGTGGCAATATCCC
 CAGGCTTCCATTCTGCCCTACTCCTGACACCTGTGGCTGGGCCATGGTGGGGCATAGCGTATGCTGGAC
 TCCTGGGAACTATTGAGCTGAAGCTAGATCTAGTGTCTAGGGCTGTGGCTGAGCTCATTCTCCCTT
 TTCTGTGGAAAGCCTGGCTGGCTGGGCTGGCAAGAGGCCCTGGCAACCCCTGTTCCCATCCCTGGGCCGTCC
 TGTACTCCTGTTGCTGGCTGGCTGTCTCTGATAGTTGTTGAGCTGAGGCCAGGGCACCCCT
 TCCTTTGGGCTATTCTGCTCTGGTTGTCAGCTTCAAGGCTCAGCTGCTCCACCTAAGCTAC
 TCACAATGCCCGCCCTGGCATTCCAGCCACAACAAACCCCCACGGCACAATGGCATATGCCCTGAGGCTTG
 GAATTGGGTTGCTTTATGTACAAGGCTAGCTGGCTTTCATGGTGGCTGAGCCAAGAATTATGGTATGGAGCTTGTGG
 CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGCTGAGCCAAGAATTATGGTATGGAGCTTGTGG
 CGCGCTGGGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTCGCCGTATGGTATCTCAAGAGCCCCGAGCCAC
 CCATGCTTTGTGCGCTGGGACTGCCCTAATGGCATTGGTACTGCTGCCACTGGGATGGCTGGGG
 CAGATGAGGCTCCCCCGCTCCGGGTCTGGCTCTGGGATCATGGTGTGAGCTGGCTGGGGCTGTAGCAGGGC
 TGGCTGTTCAAGGCTCCGCTGCTCTGGAGCAGCTGTGACAGTGCTGGTAAGGCTGGGGCAGGGCTCCAA
 GGACCAGGACTGTCTCACTCCCTCTCAGGCCCCCCTACTCTCAAGCTGACTTGGATTATGTGGCTCTCAA
 TCTACCGACACATGCAGGAGGAGTCCGGGGCGGTTAGAGAGGACAAATCTCAGGGTCCCTGACTGTGGCTG
 CTTATCAGTTGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTACCCCTGTTGGCTTCCACTTCTGCTG
 TGCGATGCCGAGCGCATCAGCCTGTTGCTCTGCTTACTGTGCCATGGCAGGCAGTCTCGGCTGGGCCCTATGGCCA
 CACAGACCTCTACTCCACAGGCCACCAGCCTGCTTCCAGGCCATCCATTGGCATGCGAGCTCGTGGGATTCC
 CAGAGGGCATGGCTCCTGACTTGGCTGCCCTTGTACTGGGAGCCAACACCTTGGCTCCACCTCCT
 TTGAGCTAGGGTGGCCACTGCTCTGCTCTGGCTTCTGTGAGAGTCAGGGCTGCCAGAGACAGCAGC
 CCCAGGGAAATGAAGCTGATGCCAGACTCAGACCCGAGGGAGGAAGAGGAGGCCACTGATGGAGATGCCCTGGGG
 ATGCCCTCAGCAGTCTGAGCAGACTGCTGCCAGGGCTCAAGTACCTCTTATCTGGTATTCTGAGATTTC
 TGGCCTGTCCTGGCAGCCTCCATCCTCGCAGGCATCTCATGGTCTGGAAAGTGTGGCTTCCCTAAGTTCATAT
 TTGAGGCTGTTGAGCTGAGCAGCTGGGACTTCTCTGGGCTAGCTTGGTGTGAGAGTGGATGGT
 CTGTGAGCTCTGGTTCAGGCAGCTATTCTGGCCAGCAGAGG**TAG**CCTAGTCTGTGATTACTGGCAGTGGCT
 ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCCTGACAGGTACTGGATGATCTGCAAGACAGGCTAGCCATAC
 TCTTACTATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATTCTATAATTCAAGGACCACAGTGGAGTA
 TGATCCCTAACTCCTGATTGGATGCATCTGAGGGACAAGGGGGGGCTCCGAAGTGGAAATAAAATAGGCCGG
 GCGTGGGTGACTTGCACCTATAATCCAGCACTTGGGAGGCCAGAGGTGGGAGGATTGCTGGTCCCAGGAGTTCA
 AGACCAGCCTGGAACATAACAAGACCCGCTCTACTATTAAAAAAAGTGAATAAAATGATAATAT

FIGURE 60

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
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MASRFSRVVLVLIDALRFDFAQPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRVVFMGDDTWKDLF
PGAFSKAFFPSFNVRDLDTVDNGILEHLYPTMDSGEWDVLIAHFLGVDHCGHKHGPHPEM
AKKLSQMDQVIQGLVERLENDTLLVAGDHGMTTNGDHGGDSELEVSAALFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLLGLPIPGFNGIVEVMAELFSGGEDSQPHSSALAQSALHLNAQ
QVSRLFHTYSAATQDLQAKELHQQLQNLFSKASADYQWLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAISPGFPFCPLLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLLGAVAAYSSFLPFLWKAAGWGSKRPLATLFPIPGPVLLLLFRLA
VFFSDSFVVAEARATPFLLGSFILLVVQLHWEGQLLPPKLLTMPRLGTSATTNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVLP
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL
LLHLLAAGIPVTTPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLCESQGLRKQQPPGNEADARVRPEEEEEP
LMEMRLRDAPQHFYAALLQLGLKYLFIQILACALAASILRRHLMVWKVFAPKFIFEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCCTGGGGACGGGCAGTCCCTGT
 GTCTCTGGGGTTGCCTAAACCTGCAAACATCACCTCTTATCCATCAACATGAAGA**ATGT**
 CCTACAATGGACTCCACCAGAGGGCTTCAGGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGT
 CCTGACAGCTCCAGAGAAGTCCAAGAGAAAATCCAGAACCTCCTGTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGACCAACCACACGCTGGTGCACCTGGCTGGAGCCGAACACTCTTACTGCGT
 ACACGTGGAGTCCTCGTCCCAGGGCCCCCTGCCGTGCTCAGCCTCTGAGAAGCAGTGTG
 CCAGGACTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTG
 CCCATATCTATTACCGTGTCTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAACACCCAGCAAATTGATTTGATTTATGGAAATGAATTGACAAAA
 GATTCTTGTGCCTGCTGAAAAAAATCGTGATTAACCTTATCACCCCTCAATATCTGGATGAT
 TCTAAAATTCTCATCAGGATATGAGTTACTGGAAAAAGCAGTGATGTATCCAGCCTAA
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG
 GGTATGCTTCGCATTGATGAAATTGGACTCTGAAGAAAACACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTCAGAACCACTGACATTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTGCAGG
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTGGGCCCG
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCCTGGTCAGTGGATCCCC
 AAACGGCAGGCTGTGATTCTTCGCTGTCAGCTCGACCAGGATTAGAGGGCTGCGAG
 CCTCTGAGGGGGATGGGCTCGGAGAGGGAGGGCTTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTGAGGAATGGGGT
 TATATGTGCAGATGGAAAAC**TGA**TGCCAACACTCCTTGCCTTGTGCAAAC
 AAGTGAGTCACCCCTTGATCCCAGCCATAAAGTACCTGGATGAAAGAAGTTTCCAGT
 TTGTCAGTGTCTGTGAGAATTACTTATTCTTCTATTCTCATAGCACGTGTGATTG
 GTTCATGCATGTAGGTCTCTAACATGATGGTGGCCTCTGGAGTCCAGGGCTGGCCGGT
 TGTTCTATGCAGAGAAAGCAGTCAATAATGTTGCCAGACTGGGTGCAGAATTATTACAGG
 TGGGTGT

FIGURE 62

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRFKELKLLTLCISIQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNLTCVHVESFVPGPPRRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILIYGNEFD
KRFFVPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSL
QEEVSTQGTILLESQAALAVLGQTLQYSYTPQLQDLDPLAQEHTDSEEGPEEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDGGLGEEGLLSRLYEEPAPDRPPGENETYLMQFMEEW
GLYVQMN
```

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGGTCTCTGCAGGGAGACGCCAGCCTGCG
TCTGCC**ATG**GGGCTCGGGTTGAGGGCTGGGACGTCCCTGCTGACTGTGGCCACGCCCT
GATGCTGCCGTGAAGCCCCCGCAGGCTCCTGGGGGCCAGATCATCGGGGCCACGAGG
TGACCCCCCACTCCAGGCCATACATGGCATCCGTGCGCTTCGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCCTGGGTGGTCTCGGCCGCCCAGTCCTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGCTGGCGCCACGTCCCTGAGTAUTGCAGGAGCCCACCCAGCAGG
TGTGGCATCGATGCTCTCACACGCACCCGACTACCACCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGCTGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGCTGCTGAGGCT
GCCAGGGAGAAGGCCAGGCCACAGGGGGACACGGTGCCGGTGGCTGGCTGGGCT
TCGTGTCTGACTTGAGGAGCTGCCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGCCACCTGACACTTACCATGCTCTGCACCCGAG
TGGGACAGCCACAGACGGGCTCTGCTGCCGACTCCGGAGGGCCCTGGTGTGCAGGA
ACCGGGCTCACGCCCTGTTCTCGGGCCTCTGGTGCAGGCCACCCAAAGACCCCGAC
GTGTACACGCAGGTGTCGCCCTTGTCGGCTGGATCTGGACGTGGTCCGGAGCAGTCC
CCAGCCCCGCCCTGCCTGGACCACCAGGCCAGGAGAAGGCC**TGA**GCCACAACCT
TGGGCATGCAAATGAGATGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCACGGG
AAGCCTGATGTTCAGGGTTGGGTGGACGGCAGCGGTGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAAATGTTAACTGACAaaaaaaaaaaaaAGAAA

FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAQIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLTLMCLTRSGDHSRRGFCSADSGGPLVCRNRAHGLVSFSGLWC GDPKT PDVY
TQVSAFVAWIWDVVRRSSPQPGPLPGTTRPPGEAA
```

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCGACTCCGGACGCCCTGACGCCCTGA
 CGCCTGTCCCCGGCCCGGC**A****TG**AGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGACGGTAG
 CAGGCGCCGCCGTGCTGCTCAAGGACTATGTCACCGGTGGGGCTGCCCCAGCAAGGCCACC
 ATCCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAAGCAGACCGCCTT
 GGAACCTGCCAGGAGAGGAGGCAACATCATCCTGCCCTGCCAGACATGGAGAAGTGTGAGG
 CGGAGCAAAGGACATCCGCGGGAGACCCCTCAATCACCATGTCAACGCCGGCACCTGGAC
 TTGGCTCCCTCAAGTCTATCCGAGAGTTGCAGCAAAGATCATTGAAGAGGGAGGAGCGAGT
 GGACATTCTAACACAACGCGGGTGTGATGCCGTGCCCCACTGGACCACGAGGACGGCT
 TCGAGATGCAGTTGGCGTTAACCAACCTGGTCACTTCTCTTGACAAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCTCGCGGATCATCAACCTCTCGTCCCTGCCCATGTTGCTGG
 GCACATAGACTTTGACGACTTGAACACTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
 GCCAGAGCAAGCTGCCATCGTCCCTTCACCAAGGAGCTGAGCCGGCGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCTGCACCCGGCGTGGCCAGGACAGAGCTGGGAGACACACGGG
 CATCCATGGCTCCACCTCTCCAGCACCAACTCGGGCCCATCTCTGGCTGCTGGTCAAGA
 GCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCGTGGCGAGGAAGTGGCGGATGTT
 TCCGGAAAGTACTCGATGGACTCAAACAGAAGGCCCCGGCCCCGAGGCTGAGGATGAGGA
 GGTGGCCGGAGGCTTGGCTGAAAGTGCCGCCTGGTGGCTTAGAGGCTCCCTGTGA
 GGGAGCAGCCCTCCCCAGA**TAA**CCTCTGGAGCAGATTGAAAGCCAGGATGGCGCCTCAG
 ACCGAGGACAGCTGCCCATGCCAGCTTCTGGCACTACCTGAGCCGGAGACCCAG
 GACTGGCGGCCATGCCAGTAGGTTCTAGGGGGCGTGCTGCCAGTGGACTGGC
 CTGCAGGTGAGCACTGCCCGGCTGGCTGGTCCGCTGCTCTGCCAGCAGGGAG
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGCCAGGGAGGAAGGGGCTC
 TGTGCACTGCAGGCCACGTCAAGGAGAGCCAGCGGTGCCTGTCGGGAGGGTTCAAGGTGC
 TCCGTGAAGAGCATGGCAAGTTGTCTGACACTGGTGGATTCTGGTCCCTGTGGACCT
 TGTGCATGCATGGCCTCTTGAGCCTGGTTCTCAGCAGTGAGATGCTCAGAATAACTG
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGG
 GGTGTTGCTGAGGGCTTGTGCCAGGCCAGCCAGAGAGCAGGTGCAGGTGTCACTCCC
 GAGTTCAAGGCTCTGCACGGCATGGAGTGGGAACCCCACCAAGCTGCTACAGGACCTGGGA
 TTGCCTGGACTCCCACCTTCTATCAATTCTCATGGTAGTCAAACACTGCAGACTCTCAAAC
 TTGCTCATT

FIGURE 66

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHLGHFLLTNLLDKLASPKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSCLAIQLFTKELSRRILQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPLEAAQPSTYLVAAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR
```

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTCGCGAGCGCTGGC**ATGT**GGT CCTGGGCGCGCTGGCGCGCTGCTGGCGGTGCTG
 GCGCTCGGCACAGGAGACCCAGAAAGGGCTGCGGCTCGGGCGACACGTTCTCGGCCTGAC
 CAGCGTGGCGCGCCCTGGCGCCCGAGCGCCGCTGCTGGGCTGCTGAGGCCTGACCTGC
 GCAGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTCTTGCA
 GAGGATTCAACAACCCCTGTGGCTAACCTCTGCTTGCAATTACTCTCATCAAACGCCCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTCCAGCCTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCTGGCCCGAGGTGTCTT
 TCAGAGAGTCAGTGGCTCTGCCATCACTGACCTGTACAGCCCCAACGGCTCTTCTCA
 CAGGGATGACTGCTCCAAGTTGGCAAGGTGGCTATGACATGGGGATTATTACCATGCC
 ATTCCATGGCTGGAGGAGGCTGTCAGTCTTCCGAGGATCTTACGGAGAGTGGAAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTGGATCACTGGCTTGTATTCCGGGCAGGAA
 ATGTTCTGCTGCCCTCAGCCTCTCAGGGAGTTCTCTCACAGCCCAGATAATAAGAGG
 ATGCCAGGAATGCTTGAAATATGAAAGGCTTCTGGCAGAGAGCCCCAACACGTGGTAGC
 TGAGGCTGTCATCCAGAGGCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGC
 TATGTCAGACCCCTGGGTTCCCAGCCACTCTCACAGATCCCTAGCCTACTGTCCTAT
 GAGACCAATTCCAACGCCAACCTGCTCCAGCCCACCGGAAGGGAGGTGATCCACCTGGA
 GCCCTACATTGCTCTTACCATGACTCGTCAGTGACTCAGAGGCTCAGAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTGAGTGGCATCAGGGAGAAGCAGTTACAAGTGGAG
 TACCGCATCAGCAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAATGGTGACCCCTAA
 CCACCGCATTGCTGCCCTCACAGGCCTGATGTCGGCCTCCCTATGCAGAGTATCTGCA
 TGGTGAACTATGGCATGGAGGACACTATGAGCCTCACTTGACCATGCTACGTACCAAGC
 AGCCCCCTCACAGAACATGAAGTCAGGAAACCGAGTTGCAACATTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA
 ATGCAGCACTGTTGGTGGAACCTGACAGGAGTGGTAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCCTGTCCTGGTGGAGATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGG
 ACAGGAATTCCCGCAGACCCCTGCAGCTCCAGCCCTGAAGAC**TGA**ACTGTTGGCAGAGAGAAC
 TGGTGGAGTCCCTGTGGCTTCCAGAGAACGCCAGGAGCCAAAGCTGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCTGGAAAGAACGCCCTGTCAGCTTGTCAGGTTCTGTCCTCGCAAATCAGAGGC
 AAGGGAGAGGTTGTTACCAGGGGACACTGAGAACATGTACATTGATCTGCCCAAGGCCACGGAA
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCTGAGAGAGGAAGTTCTGG
 AGTTCAAGATACTCTGTTGGAACAGGACATCTCAACAGTCTCAGGTTGATCAGTGGTC
 TTTGGCACTTGAACCTTGACCACAGGGACCAAGAACAGTGGCAATGAGGACACCTGCAGGAG
 GGGCTAGCCTGACTCCCAGAACCTTAAGACTTCTCCCCACTGCCTCTGCTGCAGCCCAAG
 CAGGGAGTGTCCCCCTCCAGAACATCCCAGATGAGTGGTACATTATAAGGATT
 TTTAAGTTGAAAACAACCTTCTTTCTTTGTATGATGGTTTTAACACAGTCATTAAAA
 ATGTTATAAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSGVARALAPERRLLGLLRRLYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVNVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGTTAACGTTCTGCTCCATCTCAGGAGCCCCGTCTCCCACCCCTAG
 GAAGCCACCAGACTCCACGGTGTGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG
 CGCCCAGG**ATG**CCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
 TGGCTCAAGTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGCCCTGGTCCT
 GTCTGTGGCATCTATGCAGAGTTGAGCGGAGAAATATAAAACCTTGAAAGTGCCTTCC
 TGGCTCCAGCCATCATCCTCATCCTGGCGCTGTCATGTTCATGGTCTCCTTCATTGGT
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTCTCCAAGCATTATGTACATCCTGGGAT
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
 ACTTCCTGAACGACAACATTGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAA
 AACATCATGGACTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGAGGACTACCGAGATTG
 GAGCAAGAATCAGTACCAACGACTGCAGTGCCCCCTGGACCCCTGGCCTGTGGGTGCCCTACA
 CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAATATGAC
 AAGGAGCGTTTCAGTGTGCAGGATGTCATCTACGTGCGGGCTGCACCAACGCCGTGATCAT
 CTGGTTCATGGACAACACTACACCACATGGCGTGCATCCTCCTGGCATCCTGCTTCCCCAGT
 TCCTGGGGGTGCTGCTGACGCTGTACATCACCCGGTGGAGGACATCATGGAGCAC
 TCTGTCACTGATGGCTCCTGGGCCGGTCCAAGCCCAGCGTGGAGGCCAGGCACGGG
 ATGCTGCTTGTGCTACCCAAAT**TAG**GGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCCTGTGTAGGTCCCACGCCCTGCCTC
 CCCAGGGAGCAGAGCCTGGCCTCCCTAACAGAGGCTTCCCCGAGGCAGCTCTGGAATCTGT
 GCCCACCTGGGCCTGGGAACAAGGCCCTCCTTCTCCAGGCCTGGCTACAGGGAGGGA
 GAGCCTGAGGCTTGCTCAGGGCCCATTCTACGAGGCTGCGCTTGGCGTGGTATTCAA
 GGCAGTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCCCTGGGCAGGAGGGAAGG
 GCATCTGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTTGGC
 CTCTCTCAGCCTCCAGGTGCCTTGAGCCCTTGTCAAGGGCGCTGCTCCTTGAGCCTA
 GTTTTTTACGTGATTTGTAACATTCTACAGATAAACAGGAGTTCTGAC
 TAATCAAAGCTGGTATTCCCCGATGTCTATTCTGCCCTCCCCAACAGTTGTTAA
 TCAAACAATAAAACATGTTGTTGTTAAAAAAA

FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLIIYSTVFWLIGALVLSVGIYAEVERQKYKTLESAFLAP
AIIILILLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMEELIGGVVALTFRNQTIDFL
NDNIRRGHENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIVVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLPGAKPSVEAGTGCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTCCCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
 CACCTGGGAAGATGCCGGCCCCTGGACCTTCACCCTCTGTGGTTGCTGGCAGCCACC
 TTGATCCAAGCCACCCCTCAGTCCCCTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGA
 AAAGCTGACACAGGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
 TCAGTGCCATGCCGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTAACACC
 GTCCTGAAGCACATCATCTGGCTGAAGGTATCACAGCTAACATCCTCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCTGGTCAAGACCACATCGTGGAGTTCCACATGACGACTGAGGCCAACCCATC
 CGCATGGACACCAGTGCAGTGGCCCCACCCGCTGGTCCCTCAGTGACTGTGCCACCAGCA
 TGGGAGCCTGCGCATCCAAGCTGCTGTATAAGCTCTCCTCTGGTAACGCCCTAGCTAACG
 AGGTATGAACCTCCTAGTGCCATCCCTGCCAATCTAGTGAAAAACAGCTGTGTCCCCTG
 ATCGAGGCTCCTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTAAGGTGCCATTTC
 CCTCAGCATTGACCGTCTGGAGTTGACCTCTGTATCCTGCCATCAAGGGTGACACCATT
 AGCTTACCTGGGGCCAAGTTGGACTCACAGGGAAAGGTGACCAAGTGGTCAATAAAC
 TCTGCAGCTCCCTGACAATGCCAACCCCTGGACAACATCCGTTCAGCCTCATCGTAGTCA
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCCAGAAGAATTATGGTCCCTGTTGG
 ACTCTGTGCTCCTGAGAGTGCCTGAAAGTCAAGCATGGGCTGATCAATGAAAAG
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTAAGATCCTAACTCAGGACACTCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGCCAACTGATCGTGTGGAAGTGTCCCTCCA
 GTGAAGCCCTCCGCCCTTGTTCACCCCTGGCATCGAACGCCAGCTCGGAAGCTCAGTTTAC
 ACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGGATTGGCTGGTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCCTGCTGCCGAACCAGAAATGGCAAATTAAAGATCTGGGTCCCAGTGTCAATTGGT
 AAGGCCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTGTGCTTACTCC
 AGCCTCCTGTGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
 GGAAGGCTGGTCCCAGCTGGAGTATGGGTGTGAGCTATAGACCATCCCTCTGCAAT
 CAATAAACACTTGCCTGTGAAAAA

FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAM
REKPAGGI PVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTKWFFNSAASLTMP TLNDNIPFSLIVSQDVVKAAVAAVLSPEEFMVLLDSVL
PESAHLRKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSLRIQLMNNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAAESSLTKDALVLTPASLWKPSSPVSQ
```

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAAC**ATG**GCAGCGCGTGGCGGGTTGGTGTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTGCGACGTCCTCAGCCTCTGCCAAAGAAAGAAGGAGATGGTGTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTTCCGTCGCCTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAAGTCATAGACAGTGTGCGTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC
 AAACTCCTGGCGATACTCCAGTGCATTACCAACAGGGATATTTTGCCATGGTGGATTGG
 ATGAAGGCTCTGATGTATTCAGATGCTAACATGAATTTCAGCTCCAACATTTCATCAACTTT
 CCTGCAAAAGGGAAACCCAAACGGGGTGTACATATGAGTTACAGGTGCGGGGTTTCAGC
 TGAGCAGATTGCCCGTGGATCGCGACAGAACTGATGTCATATTAGAGTGATTAGACCCC
 CAAATTATGCTGGTCCCCTATGTTGGGATTGCTTTGGCTGTTATTGGTGGACTTGTGTAT
 CCTCGAAGAAGTAATATGGAATTCTCTTTAATAAAACTGGATGGCTTGCAGCTTGTG
 TTTGTGCTTGCTATGACATCTGGTCAAATGTTGAAACCATATAAGAGGACCACCATATGCC
 ATAAGAATCCCCCACACGGGACATGTGAATTATCATGGAAGCAGTCAGCCCAGTTGTA
 GCTGAAACACACATTGTTCTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGCTTTATG
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGGCTGGTATTG
 GACTTGTGTATTATTCTCAGTTGGATGCTCTATTAGATCTAAATATCATGGCTAC
 CCATACAGCTTCTGATGAGT**TAAA**AGGTCCAGAGATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAATCGTGTGTGTTGAAAAGAAGAATGCAACTGTATATTGTATTAC
 CTCTTTTTCAAGTGATTAAATAGTTAATCATTTAACAAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAATCTGAGGTATTGAAAATAATTATCCTCTAACCTCTCTT
 CCCAGTGAACTTATGGAACATTAAATTAGTACAATTAAAGTATATTATAAAATTGTAAAA
 CTACTACTTTGTTTAGTTAGAACAAAGCTAAAACACTTTAGTTAACCTGGTCATCTGAT
 TTTATATTGCCTTATCCAAAGATGGGAAAGTAAGTCTGACCAGGTGTTCCCACATATGCC
 TGTTACAGATAACTACATTAGGAATTCTTCTAGCTTCTCATCTTGTTGTGGATGTGTAT
 ACTTTACGCATCTTCTTGTGAGTAGAGAAAATTATGTGTGTCTGTTCTGAAAATG
 GAAACACCATTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTCTCCTCCTT
 GCATATTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAGTA
 TCTCTAAATACAGGATTATAATTCTGTTGAGTATGGTGTAACTACCTGTATTAGAAA
 GATTTCAGATTCACTCCATCTCCTTAGTTCTTTAAGGTGACCCATCTGTGATAAAAATA
 TAGCTTAGTGCTAAAATCAGTGTAACTTACATGGCTAAAATGTTCTACAAATTAGAGT
 TTGTCACTTATTCCATTGTACCTAAGAGAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGGCGCAGTGACTTACGCCGTAACTCAGCACCTTGGGAGGCCAAGGCAGGCAC
 GAGGTAGGAGTTGGAGACCATCCTGCCAACATGGTGAACACCCGTCTACTAAAAATAT
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCAGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTTGAACTCAGGAGATGGAGGTTCACTGAGGCCAGATCACGCCACTGCACTCC
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVALLIVCDVPSASAQRKKEMVLSEKVSQIMEWTNKRPVIRMNGDKFR
RLVKAPPNYSIVMFTALQLHRQCVVCKQADEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPGRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFAALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLWVSVVAALALAVLAPGAGEQRRAAKAPNVVLVSDSFDRFLTDPGSQVVLPFINF
MKTRGTSFLNAYTNSPICCPSSRAAMWSGLFTHLTESWNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLRQEGRPMVNLLIRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLGLNLPHYPSPSSGENFGSSTFHTSLYWEKVSHDAIKIPKWSPLS
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNNVSLVDIYPTMLDIAGIPL
PQNLSGYSILLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS
ILPQLFDLSSDPDELTNAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWQSIG
QNYSNVIANLRWHQDWQKEPRKYENAIIDQWLKTHMNPRAV

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
GCCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTCTGGGGCTTGGGACACT
GGTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCAGCATTGTGACAG
CAGTTGGCTTCTCCAAGGGCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG
TGTGACATCTATAGCACCCCTCTGGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGAT
GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGCATGAGATGCA
CAGTCTTCTGCCAGGAATCCCGAGCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTC
ATCCTTGGAGGCCTCCTGGATTCAATTCTGTTGCCCTGGAATCTCATGGGATCCTACGGGA
CTTCTACTCACCACTGGTGCCTGACAGCATGAAATTGAGATTGGAGAGGCTCTTACTTGG
GCATTATTCTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTCTGCTCATCC
CAGAGAAATCGCTCCAACACTACGATGCCAACCAAGCCCACCTCTGCCACAAGGAGCTC
TCCAAGGCCTGGTCAACCTCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGT
ATGTG**TGA**AGAACCCAGGGGCCAGAGCTGGGGGTGGCTGGCTGTGAAAAACAGTGGACAG
CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTCAAGGTGCTGCTGAGG
ATAGACTGACTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAAACAGCATG
CAGGTTGAATTGCCAAGGATGCTGCCATGCCAGCCTTCTGTTCTCACCTGCTGCT
CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCATTCCCTTAAGCCAGGACTCAGAGG
ATCCCTTGCCTCTGGTTACCTGGACTCCATCCCCAACCCACTAATCACATCCACTG
ACTGACCCTCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTTAGCTCATTGCTGG
GGATGGGAAGGAGAAGCAGTGGCTTGTGGCATTGCTCTAACCTACTTCTCAAGCTCCC
TCCAAAGAAACTGATTGCCCTGGAACCTCCATCCACTCTGTTATGACTCCACAGTGTCC
AGACTAATTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGAAACAGAAAGCAG
GATGCAGGATGGGAGGACAGGAAGGCAGCTGGGACATTAAAAAAATA

FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPVAWNLHGILRDFYSPLVPSMKFEIGEALYLGISSLFSLIAGIILCFSCS
SQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
```

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCAGAATCTCGCTCCTGC
TTATGTGTCAAGTCTGTCTCCTCTGTGTCCAAGGGAAAGTCATCGCTCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTGAGCTCTGCTGTCTTGATTCCCTTGGCCTCACAAACGATTTGTTG
TGAAGCTGAAGGTTCAGGGTGTGAATTCCCAGTGCCACTCATCTCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTCCCTGAGAAGACATAGAAAGAAAATCAACTTCACTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAAAGTGGTTTCCAATGTACACACCTGTAAAA

FIGURE 80

MVPRIFAPAYVSVC~~LLL~~C~~P~~REVIAPAGSEPWL~~C~~Q~~P~~APRCGD~~KI~~YNPLEQCCYND~~A~~I~~V~~SLSE
TRQCGPPCTFWPCFELCCLDSFG~~L~~TND~~F~~VVKLKVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

FIGURE 81

CTCCACTGCAACCACCCAGAGCC**ATG**GCTCCCCGAGGCTGCATCGTAGCTGTCTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTT
GCTATGATGATGCCCGTGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
GTCTGCTTGAGCAGTGCTGCCCTGGACCTTCATGGTAAGCTGATAAACAGAACTGCGA
CTCAGCCGGACCTCGGATGACAGGCTTGTGCGAGTGTCACT**TAA**TGGAACATCAGGGAA
CGATGACTCCTGGATTCTCCTCCTGGGTGGGCTGGAGAAAGAGGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTGGGGCCAGAGAAACACACACTCAACTGCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGAACCCTTCACCCCT
TCTGTGAGATTTCCATCATCTCAAGTTCTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTATGTACTTTATAAATGAAAA

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLM CQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCD SARTSDDRLCRSVS

Signal peptide:

amino acids 1-24

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGCGCCCGCAGCGCTCACTCGCTCGCACTCAG
 TCGCGGGAGGCTTCCCCGCCGGCGTCCCGCCGCTCCCGACCAGAAGTTCTCT
 GCGCGTCCGACGGCAGC**ATG**GGCGTCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGA
 TCCCTGCTCTCGCTCTTCCGTGGCTCGTCCCTAGGTCCGGTGGCAGCCTCAAGGTGCG
 CACGCCGTATTCCCTGTATGTCTGTCCCAGGGGAGAACGTCACCCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTACAAGACGTGGTACCGCAGCTGAGG
 GGCGAGGTGCAGACCTGCTCAGAGGCCGGCCATCCGAAACCTCACGTTCCAGGACCTCA
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTAGGCCACGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGAACCTGACCCGTG
 GATAGCGGCCTCTACTGCTGCCTGGTGGAGATCAGGCACCACACTGGAGCACAGGGT
 CCATGGTGCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACACTGTGTGGT
 ACCCATCCTCCCTCCAGGATAAGTAAAACATCACGGCTGCAGCCCTGGCTACGGTGCTGC
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTACAAGCAAAGGCAGGCAGC
 CTCCAACGCCGTGCCAGGAGCTGGTGCAGACAGCAACATTCAAGGGATTGAAAACC
 CCGGCTTGAAGCCTCACCACTGCCAGGGATAACCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCAGCGGCAGCCTCTGAGTCTGGCGGCATCTGCTTCGGAGGCCAGCAC
 CCCCTGTCTCCCTCCAGGCCCGGAGACGTCTTCCCATCCCTGGACCCGTCCCTGACT
 CTCCAAACTTGAGGTCATC**TAG**CCCAGCTGGGGACAGTGGCTGTTGGCTGGGTCTGG
 GGCAGGTGCATTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCTGGCTCGGCCCTGGTTC
 CCTCCCTCTGCTCTGGCTCAGATACTGTGACATCCCAGAACGCCAGCCCTCAACCCCTC
 TGGATGCTACATGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTGGGTGCTGAG
 ATTCTCCCTAGAGACCTGAAATTCAACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTCAGCAGCTCTCGTTCTGAGACATGAGCCTGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGCCACCCCTCCAGGCACCAGACACAGGGCACGGT
 GAGAGACTCTCCCCGTGGCGCTTGGCTCCCCGTTGCCAGGGCTGCTCTGT
 AGACTTCCTTTGTACGACAGTGGCTCTGGGCCAGGCCTGCCACTGGCCATGCC
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTCTGAAGATCTGCAACAGGTTAAGTCAAT
 CTGGGCTTCACTGCCTGCATTCCAGTCCCCAGAGCTGGTGGCTCCGAAACGGGAAGTAC
 ATATTGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCAACCCACTGGAGATGGTGTGAGGGAGGTGGTGGGCCCTCTGGGAAGGTGA
 GTGGAGAGGGCACCTGCCCTCCCTCCACTCCACTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCCACACAATGTCTGTCCACCCCTGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTAAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pi: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCSEERRPIRNLTQDLHLHHGGHQAANTSHDLAQRHGLEASAD
HHGNFSITMRNLTLLDSGLYCCLVVEIRHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ
DSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSEGRHLLSEPSTPLSPPGPDVFFPSLDPPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCCTCTCCCTCTGCTGGACCTCCTCGTCTCTCCATCTCTCCCTCCT
 TTCCCCCGGTTCTCTTCCACCTTCTCTTCCCACCTTAGACCTCCCTGCCCTCC
 TTTCCTGCCAACCGCTGCTTCCTGGCCCTCTCCGACCCGCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCCCTTCGTCTCCCTCCGA
 CTCCGCTCCGGACCAGCGGCCTGACCTGGGAAAGG**A**T**G**TTCCCGAGGTGAGGGTCCTC
 TCCTCCTTGCTGGACTCGCGCTGCTCTGGTCCCCCTGGACTCCCACGCTCGAGCCGCC
 AGACATGTTCTGCCTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGGCCATGTGAGT
 TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCTAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCAAGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCC
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTCAGTGCCCATGAGCTGTTCCCTCC
 CGCCTGCCAACCAACCAGTGTGCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGCCTCAC
 AACCTGCCCGAACCAAGGCTGCCAGCACCCCTCCACTGCCAGACTCCTGCTGCCAACGCT
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGTGCTGGAGAAAGAGAGGGCCGGCACCCAGC
 CCCCACCTGCCCTAGGCCCTCTGAGCTTCATCCCTGCCACTTCAGACCCAAGGGAGCAG
 GCAGCACAACGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGATGGCGGG
 AAGACGTACTCCCACGGGAGGTGTGGCACCCGGCTTCCGTGCCTCGGGCCCTGCCCTG
 CATCCTATGCACCTGTGAGGATGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
 ACCCCTGCCGTACCCCGAGAAAGTGGCTGGAAAGTGCTGCAAGATTGCCAGAGGACAAA
 GCAGACCTGGCCACAGTGAGATCAGTTCTACCAGGTGCTCCAGGCACCGGGCCGGTCCT
 CGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTGCCCTGGAACACGAGG
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCAAGGCCACACAGCCAGAACTCTCCACTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTCCAGAAAGAGGCACAGCACCCGACTGCTCGCTGGCCCCCAC
 GAAGGTCACTGGAACGTCTCCTAGCCCAGACCCCTGGAGCTGAAGGTACGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAAGAC**TAA**CAGTTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAA

FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCPPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGPGTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRALEHEASDLVEIYLWKLV
KDEETEAQRGEVPGPRPHSQNLPLSDQESQEARNPERGTALPTARWPPRRSLERLPSPDPG
AEGHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25

FIGURE 87

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGAAACAGCTTGC GGCTGC GGGGAGCTCCC
GTGGCGCTCCGCTGGCTGTGCAGGCGGCCATGGATT CTTGC GGAAAATGCTGATCTCAGT
CGCAATGCTGGCGCAGGGCTGGCGTGGCTACGCGCTCCTCGTTATCGTGACCCCGGGAG
AGCGGCAGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAAGGAGCAGGGAGGAG
GCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA
CGTGGCCTGGAGGAAGAAGTGGATGGTGGCGCGAAGGC GGCGCAGCGGGAGGT CACCGT
GAGACCGGACTTGCCTCCGTGGCGCCGGACCTTGGCTTGGCGCAGGAATCCGAGGCAGCC
TTTCTCCTCGTGGGCCAGCGGAGAGTCCGGACCGAGATA CCATGCCAGGACTCTCCGGGG
TCCTGTGAGCTGCCGTGGGTGAGCACGTTCCCCAACCCCTGGACTGACTGCTTTAAGGT
CCGCAAGGCGGCCAGGGCCAGACCGAGACCGAGTGGATGTGGTA ACTGAAAGAACCAATAAAA
TCATGTT CCTCCAAAAA AAAAAAAAAAAAAA AAAAAAAAAAAAAA AAAAAAAAAAAAAA
AAAAAAAAAAA

FIGURE 88

MDSLRKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

FIGURE 89

CAGGAGAGAAGGCACCGCCCCACCCGCCTCAAAGCTAACCCCTGGGCTTGAGGGGAAGA
 GGCTGACTGTACGTTCTTACTCTGGCACCCTCTCCAGGCTGCC**ATG**GGGCCAGCAC
 CCTCTCCTCATCTGTCATGGTGGGACCCCTCCAAGGACAGCAGCACCACCT
 TGTGGAGTACATGGAACGCCGACTAGCTGTTAGAGGAACGGCTGCCAGTGCCAGGACC
 AGAGTAGTCGGCATGCTGCTGAGCTGCCGGACTCAAGAACAGATGCTGCCACTGCTGGAG
 GTGGCAGAGAAGGAGCAGGGAGGCAGTCAAGAACAGATGCTGCCACTGCTGGAG
 TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTGCCCTGTAGAGT
 TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGGAAAGAAGGAATGAGAAGTAC
 GATATGGTACAGACTGTGGCTACACAATCTCAAGTGAGATCAATGAAGATTCTGAAGCG
 ATTTGGTGGCCCAGCTGGCTATGGACCAAGGATCCACTGGGCAAACAGAGAAGATCTACG
 TGTTAGATGGACACAGAACAGACACAGCCTTGTCTTCCAAGGCTGCGTACTCACCTT
 GCCATGGCTGCCCGGAAAGCTTCCCAGTCCGGTGCCTCCCTGGTAGGCACAGGGCA
 GCTGGTATATGGTGGCTTCTTATTTGCTCGAGGCCTCCTGGAAGACCTGGTGGAGGTG
 GTGAGATGGAGAACACTTGAGCTAATCAAATTCCACCTGGCAAACCGAACAGTGGTGGAC
 AGCTCAGTATTCCCAGCAGAGGGCTGATCCCCCTACGGCTGACAGCAGACACCTACAT
 CGACCTGGTAGCTGATGAGGAAGGTCTTGGCTGTCTATGCCACCCGGAGGATGACAGGC
 ACTTGTGTCTGGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGACACACCA
 TGTCAGAGAGAACAGTGGCTGCCAGTCCGGCTTGTCTATGTGTCTATAA
 CACCCGTCTGCCAGTCGGCCCGCATCCAGTGCTCCTTGATGCCAGCAGCAGCAGCAGCAGC
 CTGAACGGGCAGCACTCCCTATTTCCCCAGATATGGTGCCTATGCCAGCAGCAGCAGC
 AACCCCCGAGAACGCCAGCTATGCCCTGGATGATGGCTACCAGATTGTCTATAAGCTGGA
 GATGAGGAAGAAAGAGGAGGAGGTT**TGA**GGAGCTAGCCTGTTTGATCTTCTCACTC
 CCATACATTATATTATATCCCCACTAAATTCTTGTCTCATTTCAAATGTGGCCAG
 TTGTGGCTCAAATCCTCTATATTTAGCCAATGGCAATCAAATTCTTCAGCTCCTTGT
 TCATACGGAACTCCAGATCCTGAGTAATCCTTAGAGCCGAAGAGTCAGGCTAACCTCAATG
 TTCCCTCCTGCTCTGCCCATGTCACAAATTCAAGGCTAACGGATGCCAGACCCAGG
 GCTCTAACCTTGATGCCAGGAGGAGCAGTCCAGCTGTCCTCTTCCACTCCTCC
 ACTTGGGAGGGAGAAATAGGAGGAGACGTCCAGCTGTCCTCTTCCACTCCTCC
 TCAGTGTCTGAGGAACAGGACTTCTCCACATTGTTGTATTGCAACATTGCA
 AGGAAAATCCACAAAAAAAAAAAAAAA
 AAAAAAAA

FIGURE 90

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLILFLLSGPLQGQQHHLVEYMERRLAALEERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPR
RDFTLAMAARKASRVRVFPFWGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTEQ
QWDTPCPRENAEAASFVICGTLVVVNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV
```

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGTCAGGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCCGCTCACGCAG
 AGCCTCTCCGGCTTCCGACCTTGAGCATTAGGCCAGTTCTCCTCTCTCTAATCCAT
 CCGTCACCTCTCCTGTCATCCGTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**
 CTCTCATGCTCAGTTGGTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTT
 GGGCCAGACAAGCCTGTCCAGGCCTGGTGGGGAGGACGCAGCATTCTCCTGTTCTGTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTCAGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAAACTGGTGAAGGATTCTATTGCGGAGGGCGCATCTCTGAGGCTGGAAAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTCCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTCAGTCCTCGGGCTGGTCCCCGGCCACAGCGAAGTG
 GAAAGGTCCACAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTTGATGTGGAGATCTCTGACCGTCCAAGAGAACGCCGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAAGGAGATACTTTTCA
 GCCTATATCGTGGCACCTGGTACCAAAGTACTGGAAACTCTGCTGTGGCCTATTTTCA
 GCATTGTTGGACTGAAGATTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACATGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTACCCGAAGCTCTGCGTTCTGATCTGAAAATGTAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAGGTG
 GCGCGTGGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTGTCTCCCG
 ATCATGGGTACTGGGCCTCAGACTGAATGGAGAACATTGTATTCACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGTCTCCTGGACTATGAGTG
 TGGGACCATCTCCTCTCAACATAATGACCAGTCCCTTATTATACCCCTGACATGCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTATAATGAGAAAATGGAACCTCC
 ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCCTTGGCAAAGGCCCTG
 AATCCCAGAGACAAGAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTCCTCCCCAGGG
 GTGAAATG**TAG**GATGAATCACATCCCACATTCTTCTTAGGGATATTAAGGTCTCTCCCA
 GATCCAAAGTCCCGCAGCAGCCGCCAAGGTGGCTCCAGATGAAGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGAGGGAAAGAAGGCTGACATTACATT
 AGTTGCTCTCACTCCATCTGGCTAAGTGATCTGAAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATTCCCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTGTTCAATTATACACTTCAGTA
 AAAAAA

FIGURE 92

MALMLSLVLSLLKLGSQWQVFGPDKPVQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGFPRPTAKWKGPQGQDLSTDRTNNDMH
GLFDVEISLTQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAEELRDAKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRLNGEHLYFTLNPRFISVFPPRKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPETSNSESSSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGCGCCGGTGGCGGTGGCGGCGGTTGCGGAGGCTTCCTGGTCGGATTGCA
 ACGAGGAGAAGATGACTGACCAACCAGCTGGCTGAATGAATGAATGGCGAGCCGAGCGC
CATGAGGAGCCTGCCAGCCTGGCGGCCCTGCCCTGTTGTGCTGCGCCGCCGCCGCC
 CGTCGCCTCAGCCGCTCGCGGGGAATGTCACCGGTGGCGGGCCGCCGGCAGGTG
 GACGCGTCGCCGGGCCCCGGTTGCGGGCGAGCCCAGCCACCCCTCCCTAGGGCGACGG
 TCCCACGGCCAGGGCCCCGAGGACCGGGCCCCCGCGCCACCGTCCACCGACCCCTGGCTG
 CGACTTCTCCAGGCCAGTCCCAGGAGACCACCCCTTTGGCGACTGCTGGACCCCTTCC
 ACCACCTTCAGGCGCCGCTCGGCCCTCGCGGACCACCCCTCCGGCGGGAACGCACTTC
 GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCCTTGACGACCACTGGCCCG
 CGCCGACCACCCCTGAGCGACCACCGTACCGCGCCACGACTCCCCGGACCCGACCC
 GATCTCCCCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGGCCCCCTC
 TTCGCCTCCTCCAGAGTATGTACTGACTGCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCACAGGGCAGTGTGAGTGTGAGGTATCAGGGCTCTGCACTGTGAAACC
 TGCAAAGAGGGCTTTACCTAAATTACACTTCTGGCTCTGCACTGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATAACCGTCAACAGG**TAA**GCAACAGAGGGTGGAACGTGAAAGTTATT
 TTATTTAGCAAGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTAACAAAG
 GAGGATGAGGGTCAAGATTACAAAATTATTTATATACTTTATTCTTACTTTATATGT
 TATATTAATGTCAGGATTAAAAACATCTAATTACTGATTTAGTTCTTCAAAAGCACTAG
 AGTCGCCAATTTCTGGATAATTCTGTAATTCTCATGGAAAAAAATTATTGAAGAAT
 AAATCTGCTTCTGAAGGGTTTCAGGCATGAAACCTGCTAGGAGGTTAGAAATGTTCTT
 ATGTTATTAATATACCATTGGAGTTGAGGAAATTGTTGTTGGTTATTTCTCTCTA
 ATCAAAATTCTACATTGTTCTTGACATCTAAAGCTAACCTGGGGTACCTAATT
 TTTAACTAGTGGTAAGTAGACTGGTTACTCTATTACAGTACATTGAGACCAAAAG
 TAGATTAAGCAGGAATTATCTTAAACTATTATGTTATTGGAGGTAATTAAATCTAGTGG
 ATAATGTACTGTTATCTAACGATTTGCCCTGTACTGCACTGAAAGTAATTATTCTTGACCT
 TATGTGAGGCACCTGGCTTTGTGGACCCCAAGTCAAAAAAACTGAAGAGACAGTATTAAAT
 AATGAAAAAAATAATGACAGGTTATACTCAGTGTAACTGGTATAACCCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCTGGCAAGTAATTCTTCACTGAGCTTGTCTTCAAG
 GTTGTGTGAAGATTAAATGAGTTGATATATAAAATGCCTAGCACATGTCACTCAATAA
 TTCTGGTTGTTAATTCAAAGGAATTATGGACTGAAATGAGAGAACATGTTAAGA
 ACTTTAGCTCCTGACAAAGAAGTGTCTTATACCTTAGCACTAAATATTAAATGCTTTA
 TAAATGATATTATACTGTTATGGAATTATGTATCATATTGTTATTAAATGTAGAAG
 AGGCTGGCGCGGTGGCTACGCCTGTAATCCTAGCATTGGGAGGCCAGGCAGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCTACTAA
 AATACAAACAAATTAGCTGGCGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCT
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCACTGAGCTGAGATCGCGCC
 GCACTCCAGCCTGGTGAGAGAGGGAGACTCTGTTAAAAAAAAAAAAAAAA

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGGLALLCCAAAAAAVASAASAGNVGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTPPAAERTS
TTSQAPTRPAPTLSTTGAPTPVATTVPAPTPRTPTPDLPSSNSVLPTPPATEAPS
SPPPEYVCNCVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTCTGGCTTG
TCTCGGTGCCAGGGCCCAGGCCGTGGTTGGGAAGACTGGACCCCTGAGCAGCTCTGG
CCCTGGTACGTGCTTGCCTGGCCTCCGGAAAAGGGCTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGTGGTGGTACCCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGCTGGGAGGGTGTGACCAGAGTGTACGGACCTGATAAAAGCGAAACTCCGGATGG
GTGTTGAGAATCCCTCAATAGCGTGCTGGAGCTCTGGTGCTGGCCACCAACTCAGAGA
CTATGCCATCATCTCACTCAGCTGGAGTTGGGGACGAGCCCTAACACCGTGAGCTGT
ACAGTCTGACGGAGACAGCCAGGCCAGGAGGCATGGGCTCTCACCAAGTGGAGCAGGAGC
CTGGGCTTCTGTACAGTAGCAGGCCAGCTGCAGAAGGACCTCACCTGTGCTCACAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCGGGCCAGCACAGCTCAGAATAAGCGATT
CACAGCA

FIGURE 96

MGGLLLAFLALVSVPRAQAVWLGRDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LT PENNLRTLSSQHGLGGCDQSVMIDLICKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

FIGURE 97

AACAGACGTTCCCTCGGGCCCTGGCACCTCTAACCCCAGACATGCTGCTGCTGCTGCC
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGCAGGAAGGCCTGTGTCCATGTGCCCTGCTCCTCTCCTACCCCTCGCAT
 GGCTGGATTTACCCTGGCCCAGTAGTCATGGCTACTGGTCCGGGAAGGGCCAATACAGA
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTGGCAGTGTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTGGGGACCCACATACCAAGAATTGACCCCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGGAGATACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTGTGAATGTGACAGCCTGACCCACAGGCCAACATCCTCATCCCAG
 GCACCCCTGGAGTCCGGCTGCCCTCAGAATCTGACCTGCTCTGTGCCCTGGCCTGTGAGCAG
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGCCCCCTGGACCCCTCCACAC
 CCGCTCCTCGGTGCTCACCTCATCCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGCCAGCGTGACCACGAACAAGACCGTCCATCTAACGTGTCCCTAC
 CCGCCTCAGAACTTGACCATGACTGTCTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCCTGTGCC
 TCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCGCTTGGGTGCACCTGAGGGATGCAGCTGA
 ATTCACTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGTGGTCGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCCCTGTCCTCTCGTCATCTCGTTGAGTGAGGTCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGGAGATA CGGGCATAGAGGATGCAAACGCTGTCAGGGTTAGCCT
 CTCAGGGGCCCTGACTGAAACCTGGGCAGAACAGACAGTCCCCAGACCAGCCTCCCCAGCT
 TCTGCCCGCTCCTCAGTGGGGAGGAGAGCTCCAGTATGCATCCCTCAGCTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCCAGTACTCGGAGATCAAGATCC
 ACAGATGAGAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA
 GAAGTCAGAGGCTGATTCTGTAGAATTAAACAGCCCTAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTATTTTTAACTAAAAGACAGACAAATTCTA

FIGURE 98

MLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPSCFSYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLISRARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSVWACEQGTPPMISWIGTSVS
PLDPSTTRSSVLTLIPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLMTVFQGDG
TVSTVLGNSSLSLPEGQSLRLVCAVDADSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVSILQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVR
CRKKSARPAAGVGDTGIEDANAVRGASQGPLTEPWAEDSPPDQPPPASARSSVGEGELOYA
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCAGTGACCTGCCGAGGTGGCAGCACAGAGCTGGAGATGAAGACCCTGTTCTG
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTCACCCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTCCGGAGGACAGGAGGCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGAAGGCCACGTTCACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT
ACATCTTTACTGCAAAGACCAGCACCATGGGGCCTGCTCCACATGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCAGGGAGGCCCTGGAAGAATTAAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTCACGCCCTGCAGACGGGAAGCTGCGTTCCGAACACTAGG
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCCTACCACAGACAGAGCCGGACCACCT
GGACCTACCCCTCCAGCCATGACCCTCCCTGCTCCACCCACCTGACTCCAAATAAGTCCT
TTTCCCCCAAAAAAAAAAAAAAAA

FIGURE 100

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTFLGVTLGLAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
```

Important features:

Signal peptide:

amino acids 1-17

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCAGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTGAG
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG
GGCGACGCTCATGCCCGCAGATGGCTCCTGACAGCAGCCCAGTGCCTCAAGCCCCGCTACA
TAGTTCACCTGGGGCAGCACAACCTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
ACTGAGTCCTCCCCCACCCGGCTCAACAAACAGCCTCCCCAACAAAGACCACCGCAATGA
CATCATGCTGGTGAAGATGGCATGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
TCTCCTCACGCTGTGTCAGTGCCTGGCACCAGCTGCCTCATTTCCGGCTGGGCAGCACGTCC
AGCCCCCAGTTACGCCCTGCCTCACACCTTGCATGCCAACATCACCATCATTGAGCACCA
GAAGTGTGAGAACGCCTACCCGGAACATCACAGACACCATGGTGTGCCCCAGCGTGCAGG
AAGGGGGCAAGGACTCCTGCCAGGGTGAECTCCGGGGCCCTCTGGTCTGTAACCAGTCTTT
CAAGGCATTATCTCCTGGGCCAGGATCCGTGCGATCACCGAAAGCCTGGTGTACAC
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAAT**TAG**ACTGGACCCA
CCCACCACAGCCCATCACCTCCATTCCACTTGGTGGTTGGCTGTTCACTCTGTTAAT
AAGAAACCTAAGCCAAGACCCCTACGAACATTCTTGGGCTCCTGGACTACAGGAGATG
CTGTCACTTAATAATCAACCTGGGTTGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTGTTCTGTTGTATCCCCAGCCCCA
AAGACAGCTCCTGGCCATATATCAAGGTTCAATAAATATTGCTAAATGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAH
CLKPRYIVHLGQHNLQKEEGCEQRTATESFPHPGFNNSLPNKHNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIIEHQKCENAYPGNITDTM
VCASVQEGGKDSCQGDGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN
```

Important features:

Signal peptide:

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTCTGCTGGAGCCG**ATGCC**AAAACCATGCATTCTTATTCA
GATTGTTTCCTTACTGCTCAGAGACAAAGAAAGAGGGAGACCGAAGAA
GTGAAAATAGAAGTTTGATCGTCCAGAAACTGCTCTAACGACAAGCAAGAAGGGAGACCT
ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCCAAATGGTTGTTCTGGTGGCAAGTCATAAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTAACCCCTTCATT
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACC GGATGCTACATTGATT
AGATTGAACTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTCAAAGCCGAGATAAACCTCTACTTGCAAAGGGATTG
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTAGAAGATATTTAAGA
AGAATGACCATGATGGTGTGGCTTCATTCTCCCAAGGAATACAATGTATACCAACACGAT
GAACTA**TAG**CATATTGTATTCTACTTTTTTTAGCTATTACTGTACTTATGTATA
AAACAAAGTCACTTCTCCAAGTTGTATTGCTATTCCCCTATGAGAAGATATTTGA
TCTCCCCAATACATTGATTTGGTATAATAAATGTGAGGCTGTTGCAAACTTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHDGDFISPKEYNVYQHDEL
```

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAA**ATG**CAGGGACCATTGCTTCTTCCAGGCCTCTGCTTCTGCTGAGCCTCTTGGAGCT
GTGACTCAGAAAACCAAAACTTCCTGTGCTAAGTGCCCCCAAATGCTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGCAGAAACTATTCACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGGCCTG**TAA**TCCCAGTTCTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAAGGAGTTGAGACCAGCCTGGCCAACATAGTGAACAC
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTGAACTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTCATTCGCGACTGCCCTCTCAGTGTTCCTGGATCCCCTCCCAAATAA
AGTACTTATATTCTC

FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTAKC^PNNASCVNNTHCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSRL

Signal peptide:

amino acids 1-18

FIGURE 107

CAAGCAGGT CATCCCTTGGTGACCTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGCAC
AGGGAAAGGGT GACCTCTGAGATTCCCCCTTTCCCCAGACTTGGAAAGTGA
CACCACATATGG****
GGCTCAGCATCTTTGCTCCTGTGTGTTCTGGGCTAGCCAGGCAGCACACCGAAGATT
TTCAATGGCACTGAGTGTGGCGTAACTCACAGCCGTGGCAGGTGGGCTGTTGAGGGCAC
CAGCCTGCGCTGCAGGGTGCCTATTGACCACAGGTGGGCTCACAGCGGCTCACTGCA
GCGGCAGCAGGTACTGGGTGCGCTGGGAAACACAGCCTCAGCCAGCTGACTGGACCGAG
CAGATCCGGCACAGCGGTTCTGTGACCCATCCGGTACCTGGGAGCCTCGACGAGCCA
CGAGCACGACCTCCGGCTGCTGCGGCTGCCGTCCCGTAACCAGCAGCGTTCAAC
CCCTGCCCTGCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGG
ATCACCAACCACCCACGGAACCCATTCCGGATCTGCTCCAGTGCCTAACCTCTCCATCGT
CTCCCATGCCACCTGCCATGGTGTGATCCCAGGAGAACATCACGAGAACATGGTGTGCAG
GCGCGTCCGGGCAGGATGCCTGCCAGGGTATTCTGGGGCCCTGGTGTGGGG
GTCCTCAAGGTCTGGTGCCTGGGGCTGTGGGCCCTGGACAAGATGGCATCCCTGG
AGTCTACACCTATAATGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAA**TGA**
CTGTTCCACCTCCACCCCCACCCCTTAACCTGGTACCCCTGCCCTCAGAGCACC
AATATCTCCATCACTCCCTAGCTCCACTCTTGTGGCCTGGAAACTTCTTGGAACTT
TAACTCCTGCCAGCCCTTAAGACCCACGAGCGGGTGAGAGAAGTGTGCAATAGTCTGGA
ATAAAATATAATGAAGGAGGGCAAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLGVLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLAAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDGGPLVCGGVLQGLVSWGSVGPGQDGIPGVYTYICKYVDWIRMMRNN

Signal peptide:

amino acids 1-17

FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
 CGCGTCCGCGAACGCCCTGGAGCCGGAGCCCCGCGCTGCC**ATG**TGCGGCGAGCTCAGCA
 ACAGGTTCCAAGGGAGGGAAAGCGTTCGGCTTGCTCAAAGCCCAGGAGAGGAGGCTGGCC
 GAGATCAACCAGGGAGTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCAGAAAA
 GCTCACAGCCTCAAAGAGAAGTACATGGAGTTGACCTGAACAATGAAGGCGAGATTGACC
 TGATGTCTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGTCAGTGACACTATATCCTACCGAGACTTGTGAA
 CATGATGCTGGGAAACGGTCGGCTGCCTCAAGTTAGTCATGATGTTGAAGGAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCC**TGA**
 GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCATAACCTCCCTCCGATCTTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCATTTGTTGGTCATTGAGGTTGTTGTGTT
 TCATCAATGTCTTGTAAAGCACAAATTATCTGCCTAAAGGGCTCTGGTCGGGAATCC
 TGAGCCTTGGTCCCTCCCTCTCTTCTCCCTCCAGGGCTCCCTGTGCAGAAGGGCTG
 ATATCAAACCAAAACTAGAGGGGCAGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
 CTCACTTGGAGGAACCAGCACTCTCCATCCTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
 CTGCAGGGCCTTTGGGTTCCCTGGACAGTGCATGGTCCAGTGCTCTGGTGTACCC
 AGGACACAGCCACTGGGCCCCGCTGCCAGCTGATCCCCACTCATTCCACACCTTTCT
 CATCCTCAGTGATGTGAAGGTGGAAAGGAAAGGAGCTTGGCATTGGAGCCCTCAAGAAGG
 TACCAAGGAACCCCTCCAGTCCTGCTCTGGCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGCAGCCCTACTGTCCCTACTGGGGCAGCAGAGGGCTCGGAGGCAGAAGTGAGGCCTG
 GGGTTGGGGAAAGGTGAGCTCAGTGCTGTTCCACCTTTAGGGAGGAGACTGAGGGGAC
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGCTGAAAAAAAAAAAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDDEENLPEKLTAFKEKYMEFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMMLGKRSAVLKLVM
MFEGKANESSPKPVGPPPERRDIASLP

FIGURE 111A

CGCGCTCCCCGCGCCTCCCTGGGCTCCACCGTCTTGCAGAGGCAGCCTCCTCCA
 GGAGCGGGGCCCTGCACACC**ATG**GCCCGGGTGGCAGGGTCGGCGCCGTGCGGCC
 CGCCTGGCCTGGCCTGGCGCTGGCGAGCGTCTGAGTGGCCTCCAGCCGTGCC
 CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGCTGGCCTCCGCGGTT
 CTCGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAAGGATC
 ACCAAGATGGACTTCGCTGGCTCAAGAACCTCGAGTCTTCATCTGGAAAGACAACCAGGT
 CAGCGTCATCGAGAGAGGCGCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
 AGAATAAGCTGCAAGTCCTCCAGAATTGCTTTCCAGAGCACGCCGAAGCTACCAGACTA
 GATTGAGTAAAACCAGATCCAGGGATCCCGAGGAAGGCCTCCGGCATCACCGATGT
 GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTCCGAGCGC
 TGCAGATTGGAGATCCTTACCCCTAACAAACAACATCAGTCGCATCCTGGTCACCAGC
 TTCAACCACATGCCAAGATCCGAACTCTGCCTCCACTCCAACCACCTCTACTGCGACTG
 CCACCTGGCCTGGCTCTGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCT
 GCATGGCTCCTGTGCATTGGAGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG
 TGCCCAGCCCCCCTCGGAGCCCCCATCCTGCAATGCAAACCTCCATCTCCTGCCCTCGCC
 CTGCACGTGCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTGATGGAGATTCCCTGCCA
 ACTTGCAGGGCATCGTCAAACATGCCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA
 GGAGCCTCACCCAGTACAAGAAACTGAAGCGAATAGACATCAGCAAGAACATCAGATATCGGA
 TATTGCTCCAGATGCCCTCCAGGGCTGAAATCACTCACATCGTGGCTGTATGGGAACA
 AGATCACCGAGATTGCAAGGGACTGTTGATGGCTGGTGTCCCTACAGCTGCTCCCTC
 AATGCCAACAAAGATCAACTGCCCTGCGGGTGAACACGTTTCAAGGACCTGAGAACCTCAACTT
 GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGCTTCCGCCCTCTGCAGT
 CCATCCAGACACTCCACTTAGCCAAAACCCATTGTGCGACTGCCACTTGAAGTGGCTG
 GCCGACTACCTCCAGGACAACCCATCGAGACAAGCGGGCCCGCTGCAGCAGCCCGCG
 ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAACGTTCCGCTGCTCAGGCTCCGAGG
 ATTACCGCAGCAGGTTCAGCAGCGAGTGCTCATGGACCTCGTGTGCCCCGAGAACAGTGTG
 TGTGAGGGACGATTGGACTGCTCCAACCAGAACAGCTGGTCCGCATCCCAAGCCACCTCCC
 TGAATATGTACCAGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
 TCTTCAAGAAGTTGCCAACCTGCGAAAATAATCTGAGTAACAATAAGATCAAGGAGGTG
 CGAGAGGGAGCTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACAGCT
 GGAGACCGTGCACGGCGCGTCTCCGTGGCCTCAGTGGCCTCAAAACCTGATGCTGAGGA
 GTAACCTGATCAGCTGTGAGTAATGACACCTTGCCTGGCTGAGTTGGTGTGAGACTGCTG
 TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCTTCACCACGTTGTCTCCCT
 GTCCACCATAAACCTCCTGTCACCCCTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
 AGTGGTTGAGGAAGAGGGGATCGTCAGTGGGAACCCTAGGTGCCAGAACCCATTTCCTC
 AAGGAGATTCCCATTCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGAGACAGTGGTGC
 TAGCTGCCAGCTGAGCCCGCGCTGCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGC
 GCAGCAACAAGGGCTCCGCGCCCTCCCCAGAGGCATGCCAAGGATGTGACCGAGCTGTAC
 CTGGAAGGAAACCACCTAACAGCGTGCCAGAGAGACTGTCGCCCTCCGACACCTGACGCT
 TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
 ACCTCTCCACTCTGATCCTGAGCTACAACCGCTGAGGTGCATCCCCGTCAAGCCTCAAC
 GGGCTGCGGCTCCGTGCGAGTGCTAACCCCTCATGGCAATGACATTCCAGCGTCTGAAGG
 CTCCTCAACGACCTCACATCTTCCCCTGCGCTGGGAACCAACCCACTCCACTGTG
 ACTGCAGTCTCGGTGGCTGCGAGTGGGTGAAGGCAGGGTACAAGGAGCCTGGCATCGCC
 CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCTGCTACCACCCAAACCCACCGCTT
 CCAGTGCAAAGGGCAGTGGACATCAACATTGTGGCAAATGCAATGCCTGCCTCCAGCC
 CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCCTGCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCATCAACACCTGCATCCAGAACCCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTCAGCTGCTCCTGCCCTC
 TGGGCTTGAAGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
 AACAAATGCCACCTGCGTGGACGGGATCAACAACATACGTGTGTATCTGTCCGCCTAATCACAC
 AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTCAAGCATG
 AGGCCAAGTGCATCCCCCTGGACAAAGGATTAGCTGCGAGTGTGTCCTGGCTACAGCGGG
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCACAAGTGCCGCCACGGGGCCAGTG
 CGTGGACACAATCAATGGCTACACATGCACCTGCCAGGGCTCAGTGGACCCCTGTG
 AACACCCCCCACCACGGTCTACTGCAGACCAGCCCAGTGCAGCAGTACGAGTGCCAGAAC
 GGGGCCAGTGCATCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACCAGGCTCGCCGG
 CCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGCAAAGACTCCTACGTGGAACCTGG
 CCTCCGCCAAGGTCCGACCCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC
 GGCATCCTCTCTACAAAGGAGACAATGACCCCCCTGGCACTGGAGCTGTACCGAGGCCACGT
 GCGGCTGGTCTATGACAGCCTGAGTTCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGA
 ATGATGGGAGTTTACAGTGTGGAGCTGGTACGCTAAACCAAGACCCCTGAACCTAGTAGTG
 GACAAGGAACCTCAAAGAGCCTGGGAAGCTCCAGAAGCAGCCAGCAGTGGCATCAACAG
 CCCCCCTCACCTGGAGGCATCCCCACCTCCACCGGCCCTCCGCCCTGCCAGGGCACGG
 ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAAACGAGCTGCA
 GACTTCAAGGCCCTCCCACACAGTCCTGGGGTGTCAACCAGGCTGCAAGTCTGCACCGT
 GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG
 GCTGGACGGGCCACTCTGCCACAGGAGGCCGGGACCCCTGCCCTGCCACAGATGCCAC
 CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCAGGGCTATGGAGG
 GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCCTGCTCAGCCTCAAGTGTACCATG
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCCTGTGCCAGCCGGCTTAGCGGC
 GAGCACTGCCACAAAGAGAATCCGTGCCCTGGGACAAGTAGTCCGAGAGGTGATCCGCC
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCATCATGGAATGTCGTGGGGCT
 GTGGGCCCTAGTGTGCCAGGCCACCCCGCAGCAAGCGCGGAAATACGTCTTCAGTGCACG
 GACGGCTCTCGTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCCTGCCCTCGCGTGTTC
CTAAGCCCCCTGCCCTGCCACCTCTGGACTCCAGCTTGATGGAGTTGGACAGCC
 ATGTGGACCCCTGGTATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAGAAGA
 AGAGAATATTAAGTATATTGTAACAAAAAAACAAAAAAATAGAACTTAAAAAAAAAAAAAAA
 AAAAAA

FIGURE 112

MAPGWAGVGA AVRRLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLDRNNITRITKMDFA GLKNL RVLHLEDNQSVIERGAFQDLKQLERLRLNK NKLQVL
 PELLFQSTPKLTRL DLSENQI QGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRILVTSFNHMPKIRTLRLHSNHL YCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL
 RGFNVADVQKKEYVC PAP HSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAI PAGAFTQYKKLK RIDISK NQISDIAPDAFQGLKS L TSIVLYGNKITEIAK
 GLFDGLVSLQLLL NANKINCLRVNTFQDLQNL NLLS LYDNKLQ TISKGLFAPLQSIQTLHL
 AQNP FVCDCHLKW LADYLQDNPIETSGARCSSPRRLANKRISQI KSKKFRCS GSEDYRSRFS
 SEC FM DLVCPEK C RCEGTIVDCSNQKL VRIPSHLPEYVTD LRLNDNEV S VLEATGIFKKLPN
 LRKINLSNNK I KEVREGA FDGA ASVQ EMLTGNQ LETV HGRVFRGLS GLKTLM RSNL ISCV
 SNDT FAGLSSVRLLS LYDNRITT ITPGAFTT LVS LSTINLLS NPNC NC HLA WL GKWL RKRR
 IVSGNPRCQKPFFLKEI PIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLR
 ALPRGMPKDVT ELYLEG NHTAVPRELSALRH LTIDLSNNSISMLTNYTFSNM SHLSTLIL
 SYNRLRCIPVHAFNGLRSLRVLT LH GNDI SSVPEGSFNDLTSLSHLALGTNPLHCDCSRWL
 SEWVKAGYKEPGIARCSSPEPMADRLLTTPTHRFQCKGPVDINIVAKCNACLSSPCKNNGT
 CTQDPVELYRCACP SYKGKDCTVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCPLGFEGQR
 CEINPDDCEDND CENNATCVDGINNYVCICPPNYTGE LCDEVIDHCVPELNLCQHEAKC I PL
 DKGF SCECVPGYSGKL CETDNDDCVAHKCRHGAQCVD TINGYTC TQPQGFSGPFCEHPPP MV
 LLQTSPCDQYECQNGAQCIVVQQEPTCRCPPGFAGPRCEKLITVNFGKDSYVELASAKVRP
 QANISLQVATDKDNGILL YKGDN DPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDQFHS
 VELVTLNQTLNLVVDKGTPKSLGKLQKPAVGINSPLYLGGI PTSTGLS ALRQGTDRPLGGF
 HGC IHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVCECRPGWTGPLC
 DQEARDPCLGHRCHHGKVATGTSYMCKCAEGYGGDLC DNKND SANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVI RRQKG YASCATASKV PIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCTGAGCTGCCTGTCAACGACTAGGTGGAGCAGTGTTCCTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTCAGTCTGTCT
CCGGCAGGCTTGAGG**ATGA**AGGCTGCCGGCATTCTGACCCCTATTGGCTGCCGTGGCACAG
GCGCCGAGTCCAAAATCTACACTCGTGCAAACGGAAAAATATTCTCGAGGGCTGCCGTG
GACAATTACTGGGCTTCAGCCTGGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA
AACACACCACAGCCCCGACGGCCTGGATGACGGCAGCAGCGACTATGGCATCTTCAGATCA
ACAGCTTCCGCGTGGTGCAGACGGAAAGCTGAAGGAGAACAAACCAACTGCCATGTCGCCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACATTGGCAAGGCTGGAAGAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAGGCTGTGAGGTTCC**TAA**ACTGGAACCTGGACCCAGGATGCTTGCAGCAAC
GCCCTAGGATTCAGTGAATGTCAAATGCCGTGTCATCTTGTCCCCTTCCCAATA
TTCCTTCTCAAACCTGGAGAGGGAAAATTAGCTATACTTTAAGAAAATAATTTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTLLIGCLVTGAESKIKYTRCKLAKIFSRAGLDNWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCCHVACSAITDDLTDAIICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

FIGURE 115

CAGGCCATTGCATCCCACTGTCCTGTGGAGGCCAGGCCACACCGTCCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCTATTAAAACCTGTACATGGCTCCC
 CATTGGTTTGAGAAAAGTTCAAGCTTTACCTTGGTGTGCCTGTATCCCAGTGTTC
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTACTGTCACCTCCAGATCTGCTCTCAC
 CAAGAGAGATTCTTCTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTAAGGAA
 ACATTCAAGTCCCTGTCACATAGACCCCTGATGTCCTCATCCATCTCAAATGTCACCAG
 CTTTGACTCAGTTGTCCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAATTCTGC
 TGCTCTCCATCAACAGATAAGGAAAGGAAAGAAAAATCTGACTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAAGATTGACATCCAAGATTGGAGAGGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCCTGGAGATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
 AGTCCGACCTTGGCCAGTATGTGACCTTCTGAGGTCTTCTCAGACAAACAGAAAATCTCC
 CTCCCTCACAGCTGCACGTGTGCTTACACACCAAGCAATGAGCACTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAACCGGGTGGACCCCTGGAGT
 CCATTGACCACAGTGTACAGGGTTCTGTGAGCCTGACCCGGTGCACCTCTCAGAAGCA
 ATAGAAAAGTTCATCCGTGAAACCTCCTAAAAGCCACCATGGGCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAATTTCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGTA**TAA**TCAGATTGTTTAAGATCTCATTAAATGTCATTGTTATGGATTGTAGACC
 CAGTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTAAAAATAAA
 CTTGAGTCTGAATGTGAGCCACTTCCTATATACCACACCTCCCTGCCACTTTAGAAA
 AACCATGTCTTTATGCTATAATCATTCCAAATTGCTGAGTGTAAAGTTACAAATGTGGTG
 TCATTCCATGTTCAGCAGAGTATTTAATTATTTCTCGGGATTATTGCTCTGTCTA
 TAAATTGAAATGATACTGTCCTTAATTGGTTTCAAGTTAAGTGTGTATCATTATCAA
 AGTTGATTAATTGGCTTCAGTATAATGAGAGCAGGGCTATTGTAGTCCAGATTCAAT
 CCACCGAAGTGGTCACTGTCATCTGTTAGGAAATTTGTTGTCCTGTCTTGCCTGGATC
 CATAGCGAGAGTGCTCTGTATTTTAAGATAATTGTATTTGCACACTGAGATATAA
 TAAAAGGTGTTATCATAAAAAAAAAAAAAAA

FIGURE 116

MPLLKLVHGSPLVFGEKFKLFTLVSACIPVFRALARRKILFYCHFPDLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAASFKEFKSLSHIDPDVLYPSLNVTSDSVVPEKLD
DLVPKGKKFLLLSINRYERKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIKEFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGCGGCAGAACCAATGTTGGACTTCGCGATCTT
 CGCCGTTACCTTCTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTCCAGAC
 AAGCTGCAGGAATTCCAGGGATTACTCCAAC TGAAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAAAGTTGCATGAGTTCTGGTTAATTGCATGAGAGATATGGCCTGTGGT
 CTCCTCTGGTTGGCAGGCAGCTCGTGGTAGTTGGCACTGTTGATGTACTGAAGCAGC
 ATATCAATCCAATAAGACATCGGACCCTTGAAACCAGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAAC TTGCCCTCCTCCTAAAGCTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGTAGTACATTGAAGATGATCAGGAAGTCATTG
 CTTCCAGAAGAACATGGCACAGTTGGTCTGAGATTGGAAAAGGCTTCTAGATGGGTAC
 TTGATAAAAACATGACTCGGAAAAAACATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTCTG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGCAATCTGTTTTAACCACCTCTGAA
 GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTGGAAATGGCCTTTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTGTGAAACTGTTGAACTGCCA
 AACTGACTCCAGTTCTGCCAGCTCAAGATATTGAAGGAAAATTGACCGATTATTATT
 CCTAGAGAGACCCTCGCCTTATGCCCTGGTGTGGTACTTCAGGATCCTAATACTGGCC
 ATCTCCACACAAGTTGATCCAGATCGGTTGATGATGAATTAGTAATGAAAATTTCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTGCATATATGGTACCC
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTCTGAGGGACAGGTTATTGA
 AACAAAGTATGAACGGTAACATCATCAAGGGAAGAACGCTGGATCACTGTCTCAAAGAGAT
 ATTTAAAATTTCATACATTAAAATCATTGTTAAATTGAGGAAAACAACCATTAAAAA
 AAATCTATGTTGAATCCTTTATAAACCAAGTATCAGTTGTAATATAAACACCTATTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVSLGTVDVLKQHINPNKTSDPFETMLKSLLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQE VIRFQKNHGTWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL
QDPNTWPSPHKFDPDRFDELVMKTFSSLGFSGTQECPELRFAYMVTIVLLSVLKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTGTCGGCTTGC~~GGGG~~GACTTCAGGAGTCGCTGTCTGAAC~~TCCAGCCTCAGA~~
GACCGCCGCC~~CTTG~~CCCCGAGGGC~~CA~~**TG**GGCCGGTCTCAGGGCTTGTGCCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTACACCTTATTCTGGTCCC~~GG~~A~~CAGCAACAT~~
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATT~~CAGCTGG~~
TGGCCGCGCTCTGT~~C~~ACCC~~T~~GGGC~~C~~CTTTGCAGTGGAGCTGGCCGGTT~~C~~CTCAGGA
GTCTCCATGTTAACAGCACCCAGAGCCTCATCTCCATTGGGCTCA~~T~~GTAGTGCATCCGT
GGCC~~C~~CTGT~~C~~CTT~~C~~TCATATT~~C~~GAGC~~G~~TTGGGAGTGC~~A~~CTACGTATTGGTACATT~~TT~~GTCT
TCTGCAGTGC~~C~~CTT~~C~~CCAGCTGTCA~~T~~GAAATGG~~C~~TTATT~~C~~GTACC~~G~~T~~TT~~GGG~~C~~TGAAA
AAGAAACCC~~TT~~**TG**AATTAC~~CT~~TCATGAC~~GG~~GAAC~~CT~~AAGGACGAAGC~~C~~TACAGGGGCAAGGG
CCGCTTC~~G~~TATT~~C~~CT~~G~~GAAGAAGGAAGGC~~A~~TAGG~~C~~TT~~G~~GGTTTCCC~~C~~TC~~G~~GA~~A~~ACTG~~C~~TC
TGCTGGAGGATATGTGTT~~G~~GAATAATTACGT~~CT~~TGAGTCTGGGATTATCCG~~C~~ATTGTATT~~TA~~
GTGCTT~~G~~TAATAAAATGTTTG~~A~~CTAACATTAAAGACTTATACAGTTAGGGGACA
ATTAAAAAAA

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 121

TCCCGGACCTGCCGCCCTGCCACTATGTCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGGAAAGGCCCTGGCATCAGAGTGCAGCCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCAGTGGCTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACTTCACGGGTGC
CCACTCAGGTCACTTATGAAACCCATGTCCATTGGCATCAGCTTCATGGCAACTACATGG
ATCGGGTGCCACACCCAGGCCATCGGGCAGCCCAGGGTCTACTGGCCTGCAGGTGGCT
CAGGGAGCCCTGAGGTCCAATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGCCACACTACCGCTCCCCTGAGGCC
CTGCTGATCCGCACCCATTCCCTCCCATGGCAAAAACCCACTGTCTCCTCTCCA
ATAAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTILGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAAG**ATG**CAACT
 GACTCGCTGCTCGTGTCTGGTCAGGGTAGCCTCTATCTGGTCACTGTGGCCAGG
 ATGATGGTCTCCCGCTCAGAGGACCTGAGCGTATGACCACGAGGCCAGCCCCGGCC
 CGGGTGCCTCGGAAGCGGGCACATCTCACCTAACGCCCAGGCCATTCCACTCT
 CCTAGGGCTGCTGGCCCCGCTGGGAGGCTTGGGCATTCTGGCAGCCCCCAACGCC
 CGAACACAGCCCCCACCTCAGCCAAGGTGAAGAAATCTTGGCTGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCTGAACCTGCTCGTCACAGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTCCCCCAGTAAAGCTGTAGAGTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAATCTCAACTGCCGGATGGAGTGGAGAACGGTACAACGGGCCGGACCTC
 GCTTGACCCACGCCAGCCAAGATCTGCTCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCCAGCCCTCAAAGTCGTCTGTCTACATGCCCTCTACAGCACGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACATACCATAGTGATAACCCCTACTACCCATC
 TGGG**TGA**CCCAGGGCAGGCCACAGAGGCCAGGGCAGGGCTGGAAGGACAGGCCTGCCATGC
 AGGAGACCATCTGGACACCAGGGCAGGGAAAGGGTTGGCCTCAGGCAGGGAGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGCCAGGCCAAGTCTCAAGTGGCAGAGAACGGTCCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCAGGGAGGAGTGGCT
 CTCTGTGCAGCCTCACAGGGCTTGCCACGGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGAGGAAGCTAACGCCCTGGTT
 CTTGCCATCCTGAGGAAAGATAGAACAGGGAGGGGAGATTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGTGGGC
 CAGAGGAGCTCCAGCCCTGCCTAGTGGCGCCCTGAGCCCTTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTCCAAAATCCCTTCTGCCAGTACTCCCCCTGTACCAACCCATT
 GCTGATGGCACACCCATCCTTAAGCTAACAGACAGGACATTGTGGCCTCCACACTAACGCC
 ACAGCCATCCCGTGCTGTGTCCCTTCCACCCCAACCCCTGCTGGCTCCTCTGGAG
 CATCCATGTCCCAGAGGGTCCCTAACAGTCAGCCTCACCTGTCAGACCGGGTTCTCC
 CGGATCTGGATGGCGCCGCCCTCAGCAGCGGGCACGGTGGGCCGGCGCAGA
 GCATGTGCTGGATCTGTTCTGTGTCTGTCTGGTGGGTGGGGAGGGAGGGAAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTGTGAAGAACATCGTGTCTTGGAGCAGGAAATAAGCTT
 GCCCCGGGGCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSILVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPSAKVKKIFGWGDFYSNIKTVANLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKCPDNYHSDTPY
YPSG
```

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTGATGACTTCAGATGTCTAGGAACCAGAGTGGTGCAGGGGCCCA
 GGCAGGGCTGATTCTGGCGGAGGAGTAGGGTAAAGGGTCTGCATGAGCTCCTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGAGACTTGACTTCAAGCCACAGAAT
 TGGTCCAAGTGTGCGCGCCGCCGCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
 CATCTTCCCAGCACCAGGATCCCGGGTAGGAGGCAGCGGGGAGCACAGGCCAGCC
 GGCTGCGGCTGCCACACGGCTCACCATGGGCTCCGGCGCCGGCGCTGTCGCGGTGCG
 GCCGTGCTGCTGGTCTCACGCTGCCGGGCTGCCGTCTGGGACAGAACGACACGGAGCC
 CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGCAGTCGAACCCGCCACGGACTCCAAGG
 GCTCCTCTCCTCCCCGCTGGGATATCGGTCCGGCGGCCACTCCAAGGTGCCCTCTCG
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATATTACTT
 CGATCAGATCCTGGTGAATGTGGTAATTTTCACATTGGAGTCTGTCTTGAGCACCAA
 GAAAAGGAATTTACAGTTCAGTTCACGTGATTAAAGTCTACCAGAGCCAAACTATCCAG
 GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCCTTGCGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGCCTGCTCACCTAGATAAAGAGGATAAGGTTACCTAA
 AACTGGAGAAAGGTAAATTGGTGGAGGCTGGCAGTATTCCACGTTCTGGCTTCTGGT
 TTCCCCCTATAGGATTCAATTCTCCATGATGTTCATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTCATCATTGGATTGATGTTCTGGTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGCTGAACCAATACAAATTCACAGATTATTGTG
 TGTGTCTGTTCACTATTTGGATTGGACTCTAACGAGATAATACCTATGCTAAATGTA
 ACAGTCAAAAGCTGCTGCAAGACTTATTCTGAATTCATTCCCTGGATTACTGAATTAGT
 TACAGATGTGAAATTATTGTTAGTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTACTG
 TGTTAATATATTGATTATTTGTTTATTCCCTTGGATTAGTTGTTGGTTCTGTAA
 AAAACTGGATTTTTTCACTGAACTGGTATTATGTTCTCTAAAATAAGGTAATGAA
 TGGCTTGCCCACAAATTACCTTGACTACGATATCATCGACATGACTCTCTCAAAAAAAA
 GAATGCTTCATAGTTGATTTAATTGTATATGAAAGAGTCATATTCCAAAGTTATATT
 TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAGTTGCTTACCCAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTACTTATTGC
 TCAACTTAATTAAATGATTGATAATAACCACCTTATTAAAAACCTAACGGTTTTTT
 TCCGTAGACATGACCACTTATTAAACTGGTGGTGGGATGCTGTTCTAATTACCTAT
 TTTCAAGGCTCTGTTGATTGAAGTATCATCTGGTTGCCTTAACCTTTAAATTGTA
 TATATTATCTGTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTAGTGCACATAT
 CTTGTCTTTGTATAGGTACATGAATTACAAATTATTATGCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAAA

FIGURE 126

MGSGRRALSAVPAVLLVLTPGLPVWAQNDTEPIVLEGKCLVVCDNSNPATDSKGSSSPLGI
SVRAANSKVAEFSAVRSTNHEPSEMSNKTRIYFDQILVNVGNFITLESVFVAPRKGIYSFSF
HVIKVYQSQTIQVNMLNGKPVISAFAGDKDVTREAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

FIGURE 127

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTCGGCTGCGCCTTCATTGCCTTCGGCCTGCGCTC
GCCCTTATGTCTTACCATGCCATCGAGCCGTTGCGTATCATCTTCCTCATGCCCGGAGC
TTTCTTCTGGTTGGTGTCTACTGATTCGTCCTTGTTGGTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTGGAGCGTTGTCTGTGTC
TATATCCAAGAAATGTTCCGATTGCATATTATAAACTCTTAAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCCAGGTGAGACAGCACCCCTATGCGACTGCTGGCTATGTTCTGGCT
TGGGCTTGGAAATCATGAGTGGAGTATTCCTTGTGAATACCCTATCTGACTCCTGGGG
CCAGGCACAGTGGCATTCATGGAGATTCTCCTCAATTCTCCTTATTCAAGCTTCATGAC
GCTGGTCATTATCTGCTGCATGTATTCTGGGCATTGTATTTTGATGGCTGTGAGAAGA
AAAAGTGGGCATCCTCCTATCGTTCTCCTGACCCACCTGCTGGTGTCAAGCCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGTCACTGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTGCCAAG
ACAAGAACTTCTTACAACCAGCGCTCCAGA**TAA**CCTCAGGGAACCAAGCACTCCCAA
ACCGCAGACTACATCTTAGAGGAAGCACAACGTGCCTTTCTGAAAATCCCTTTCTG
GTGGAATTGAGAAAGAAATAAAACTATGCAGATA

FIGURE 128

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKW
GILLIVLLTHLLVSAQTFISSIONYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCILLCQDKN
FLLYNQRSR
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCC**ATG**TTTCGCTCTGGGCTTGCCTTCT
 TGGTGTCTTGGTGGCTCGGTGAGAGCCATCTGGGGGTTCTGGGGGCCAAGAACGTCTCGCAGAAAGACGCC
 AGTTTGAGCGCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGACCC
 GCAACAGGACAGAGGGCGTGCCTGTTGTAACAGTCTGAACAAGCAGAAGGGGGCGCCGGTGTGTTGTGG
 TCGCCAGAAGGAGGCTGTGGTGTCTCCAGGTGCCCTAATCCTCGAGGGATGTTCAGCGCAAGTACCTCT
 ACCAAAAAGTGAACGAACCCGTGTCAAGCCCCCACCAGAATGAGTCGGAGATTCACTTCTACGTGGATG
 TGTCACCCGTCAACAGTCAACACCATACCAAGCTCCGGTCAGCCGATGGACGATTGTGCTCAGGACTG
 GGGAGCAGTTCAGCTCAATACCAACAGCAGCACAGCCCAGTACTTCAGTATGAGTCCCTGAAGGGTGGACT
 CGGTAAATTGTCAGGTGACCTCCAACAAGGCCCTCCCTGCTCAGTCATCTCATTAGGATGTGCTGTGCTG
 TCTATGACCTGGACAACAACGTAGCCTCATCGGATGTACCAAGACGATGACCAAGAAGGGGCCATACCGTAC
 AGCGCAAAGACTCCCCAGCAACAGCTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCCGGGCT
 CCCTGCCCTTCTACCCCTCGAGAAGATGAACCGTCGATCAAGGGCACGCCAGAAAACCCGTCACTGCTGG
 TGTCTCAAGCAGTCACGTCTGAGGCATACGTCACTGGGATGCTCTTGCCTGGTATATTCTCTCCTTTACC
 TGCTGACCGTCTCCTGCCCTGCTGGAGAAGTGGAGGAGAAGAAGAAGACCTGCTGGTGGCATTGACCGAG
 CCTGCCAGAAGCGGTACCCCTCGAGTCTGGTCAATTCTTCCCTGGCAGTCCCCATTGAGGTTACAAC
 ATGGCTCCTTGAGAATGTTCTGGATCTACCGATGGTCTGGTGAACAGCGCTGGCACTGGGACCTCTTAC
 GTTACCAAGGGCGCTCCTTGAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGATG
 ACTACGACACATTGACCGACATCGATTCCGACAAGAATGTCATTGCAACAGAACATACCTCTATGTGGCTGAC
 TGGCACGGAAGGACAAGCGTGTCTCGGGAAAAAGTACCAAGATCTACTCTGGAACATTGCCACATTGCTGT
 TCTATGCCCTCTGTGGTGCAGCTGGTATCACCTACCAAGACGGTGGTGAATGTCACAGGAATCAGGACATCT
 GCTACTACAACCTCCTCGGCCAACCCACTGGCAATCTCAGCGCCTCAACAAACATCCTCAGCAACCTGGG
 ACATCCTGCTGGGCTGCTTCTGCTCATCACCTGCAACCGGGAGATCAACCAACCAACCGGGCCTGCTGCC
 ATGACCTCTGTGCCCTGGAATGTGGGATCCCCAACACTTGGCTTCTACGCCATGGGACAGCCTGATGA
 TGGAGGGGCTGCTCAGTGCTGCTCATGTCATGTCAGCTGGCCAACTTACAAATTTCAGTTGACACATCGTT
 ACATGATCGCCGACTCTGCATGCTGAAGCTTACCAAGCGGCCAGCGACATCAACGCCAGCGCTACAGTG
 CCTACGCCCTGCCATTGTCATCTTCTCTGTGCTGGCTGGTCTTGGCAAAGGGAACACGGCGTTCT
 GGATCGTCTTCCATCATTACATGCCACCCCTGCTCCTCAGCACGCGACTCTATTACATGGGCCGGTGG
 AACTGGACTCGGGGATCTTCCGCCATCCTCCACGTGCTCTACACAGACTGCACTCCGGCAGTGCAGCGGCC
 TCTACGTGGACCGCATGGTCTGCTGGCATGGCAACGTCATCAACTGGTCTGGCTGCCTATGGGCTTATCA
 TGCGCCCAATGATTCGCTTCTACTTGTGGCCATTGGCATCTGCAACCTGCTCTTACTTCGCTTCTACA
 TCATCATGAAGCTCCGGAGTGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCACTGTTGCACCTCCGGTGG
 GGGCTTCGCGCTCTTCTTCTCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAAGAGTCGAGGGAGCACA
 ACCGGGACTGCATCCTCCGACTTCTTGACGACCACGACATCTGGCACTTCTCTCCATGCCATGTC
 GGTCTTCTGGTGTGCTGACACTGGATGACGACCTGGACTGTGCACTGGGACAAGATCTATGTCCTC**TAGC**
 AGGAGCTGGGCCCTCGCTCACCTCAAGGGCCCTGAGCTCCTTGTCATAGACCGGTCACTCTGCTGCT
 GTGGGGATGAGTCCCAGCACCGCTGCCAGCACTGGATGGCAGCAGCACGCCAGGTCTAGCTTAGGCTTGGC
 GGGACGCCATGGGTGCCATGGAACCTTGCAGCTGCCCTCTGCCAGGGAGCAGGCCCTGCTCCCTGGAAACCCCC
 AGATGTTGGCCAATTGCTGCTTCTCTCAGTGTGGGCCCTTCCATGGGCCCTGTCCTTGGCTCTCCATT
 GTCCCTTGTCAAGAGGAAGGAGTGGAGGGACACCCCTCCCATTTCATGCCCTGCAATTGGCCCGTCCCTCCCC
 ACAATGCCCGCAGCTGGACCTAAGGCCTCTTCTCTCCATACTCCACCTCAGGGCTAGTCTGGGGCTGA
 ATCTCTGTCTGTATCAGGGCCCCAGTCTCTTGGCTGCTGCCATCTGCCATTCCAGTCAGCC
 AGGATGGATGGGGTATGAGATTGGGGTGTGGCCAGCTGGTCAAGCTTGTGCTAAGGCCCTGCAAGGG
 CCTGGGGCAGTGCCTATTCTCTTCCCTGACCTGTGCTCAGGGCTGGCTCTTAGCAATGCGCTAGCCAAATT
 TGAGAACGCCCTCTGATTCAAGAGGCTGAATTCAAGGGCTCACCTCTCATCCCATCAGCTCCAGACTGATGCC
 AGCACCAAGGACTGGAGGAGAAGGCCCTCACCCCTCCCTCTTCCAGGCCCTAGTCTGCCAAACCC
 AGCTGGTGGCCTTCAGTGCCTGACACTGCCAAGAATGTCAGGGGAAAGGAGGGATGATACAGAGTTCA
 CCCGTTCTGCCCTCACAGCTGTGGCACCCAGTGCCTACCTTCAAGAAAGGGCTTCAGGAAGGGATGTGCT
 CCTCTACGTGCCAGTCTAGCCTGCTCTAGGACCCAGGGCTGGCTCTAAGTTCCGCTCAGTCTCAGGCC
 AGTCTGTGTTAGTCATGCACACACATACCTATGAAACCTTGGAGTTACAAAGAATTGCCCAAGCTCTGGC
 CCTGGCCACCCCTGGTCTGGATCCCTCGTCCCACCTGGTCCACCCAGATGCTGAGGATGGGGAGCTCAGG
 CGGGGCTCTGCTTGGGATGGGAATGTGTTTCTCCAAACTTGTGTTTATAGCTCTGCTTGAAGGGCTGG
 AGATGAGGTGGGTCTGGATCTTCTCAGAGCGTCTCCATGCTATGGTGCATTCCGTTATGAATGAATT
 TGCATTCAATAAACCAACAGACTCAAAAAAAAAAA

FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNNTYQLRVSRMDDFVLRTGEQFSFNTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFPCSVISIQDVLCPVYDLDNNVAFIGMYQTMTKKAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPVQDQGHROKTLSDLVSQAVTSEAYVSGMLFCLGIIFLSFYLL
TVILLACWENWRQKKKTLLVAIDRACPESGHPRVLADSFPGSSPYEGYNYSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLDIDSDKNVIRTKQYLYVADL
ARKDKRVLRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLIIILQREINHNRAALLRNDCALECGIPKHFGFYAMGTALM
MEGLLSACYHVCPTYNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIIIIATLLLSTQLYYMGRWKLDGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLILYFAFYIIMKLRSGERI
KLIPLLICIVCTSVVWGFALFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDDTVQRDKIYVF
```

Important features of the protein:

Signal peptide:

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCTGCCCTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGGAGC
TCTCTTCTTGCTGGCAGCTGGACCAAGGGAGCCAGTCTTGGCGCTGGAGGGCCTGTCCTG
ACC**ATG**GTCCCTGCCTGGCTGTGGCTGCTTGTGCTCCGCCCCCAGGCTCTCCCCAAGGC
CCAGCCTGCAGAGCTGTGTGGAAAGTTCCAGAAAACATATGGTGAAATTCCCTTATACC
TGACCAAGTTGCCGCTGCCCGTGGAGGGGCTGAAGGCCAGATCGTGTGTCAGGGACTCA
GGCAAGGCAACTGAGGGCCATTGCTATGGATCCAGATTGGCTCCTGCTGGTGACAG
GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAAGCTACAGGTACCCCTGGAGATGCAGGATG
GACATGTCTTGTGGGTCACAGCCTGTGCTGACGTGAAGGATGAGAATGACCAAGGTG
CCCCATTCTCAAGCCATCTACAGAGCTGGCTGAGCCGGGTACAGGCTGGCATCCC
CTTCCTCTCCTTGAGGCTTCAGACCAGGATGAGCCAGGCACAGCCAACCTGGATCTTCGAT
TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTCCCCAGACATGTTCCAGCTGGAGCCTCGG
CTGGGGCTCTGCCCTCAGCCCCAAGGGGAGCACCAGCCTGACCACGCCCTGGAGAGGAC
CTACCAAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACAGGCCACTG
CCACCGTGGAAAGTCTCCATCATAGAGAGCACCTGGGTGTCCTAGAGCCTATCCACCTGGCA
GAGAATCTCAAAGTCTATACCCGACACATGGCCAGGTACACTGGAGTGGGGTGATGT
GCACTATCACCTGGAGAGCCATCCCCGGACCTTGAAGTGAATGCAGAGGGAAACCTCT
ACGTGACCAGAGAGCTGGACAGAGAACGCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
AATTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTATGGATGAGAA
TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
CAGGTACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAATGCAGAGGGAAACCTCT
CACGTTGTGATCAGCTCTGAGCCCTGAGCCTGAGGATGGGTAGAGGGAGAGCCTTCCA
GGTGGACCCCACCTCAGGCAGTGTGACGTGGGGTCTCCACTCCAGCAGGCCAGAACAA
TCCTGCTCTGGTGTGGCCATGGACCTGGCAGGGCAGAGGGTGGCTCAGCAGCACGTGT
GAAGTCGAAGTCGCACTAGATATCAATGATCACGCCCTGAGTCATCACTTCCAGAT
TGGGCTATAAGCCTCCCTGAGGATGTGGAGCCGGACTCTGGTGGCCATGCTAACAGCA
TTGATGCTGACCTCGAGCCGCCCTCGCCTCATGGATTGGCATTGAGAGGGAGACACA
GAAGGGACTTTGGCCTGGATTGGAGCCAGACTCTGGCATGTTAGACTCAGACTCTGCAA
GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGCAGAGTGTGGCGA
AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACGCCACGGTGAAGTGTGCTAGTGGAGAGA
GTGATGCCACCCCCCAAGTTGGACCAAGGAGAGCTAGAGGCCAGTGTCCCCATCAGTGCC
AGCCGGCTTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCT
CCCTAGTCATGACTCAGAGGGCTGGCTGCATTGAGAAATTCTCCGGGAGGTGCACACC
GCCAGTCCCTGCAGGGGCCAGCCTGGGGACACCTACACGGTGTGCTGGAGGCCAGGA
TACAGCCCTGACTCTTGCCTCTGTGCCCTCCAAATACCTCTGCACACCCGCCAGAACCATG
GCTTGTGAGTGGACCCAGCAAGGACCCGATCTGGCAGTGGCAGTGGCAGGGTCCCTACAGC
TTCACCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCTCCAGACTCTCAATGGTC
CCATGCCCTACCTCACCTGGCCCTGCATTGGTGAGCCACGTGAACACATAATCCCCGTGG
TGGTCAGCCACAATGCCAGATGTGGCAGCTCTGGTGTGAGTGTGATGTGTCGCTGCAAC
GTGGAGGGCAGTGCATGCGCAAGGTGGCCGATGAAGGGCATGCCACGAAGCTGTGGC
AGTGGCAGTCTGTAGGCACCCGGTAGCAATAGGAATCTCCTCATCCTCATTTCACCC
ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAAGCAGACAGCGTCCCCCTGAAGGGC
ACTGT**TGA**ATGGCCCAGGCAGCTAGCTGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC
CTGGGAGAGAGGCCAGCACCAAGATCCAGCAGGGACAGGACAGAGTAGAAGCCCTCCAT
CTGCCCTGGGGTGGAGGCACCATCACCATCACAGGCATGTGTCAGAGCCTGGACACCAAC
TTTATGGACTGCCCATGGAGTGTCCAATGTCAGGGTGTGCCCCAATAAAAGCCCCA
GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAG

FIGURE 132

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPFLYLTKLPLPREGAEGQIVLSGDSG
KATEGPFAMDPDSGFLLVTRALDREEQAELYQLQVTLEMQDGHVLWGPQPVLHVVKDENDQVP
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRL
GALALSPKGSTS LDHALERTYQLLVQVKDMGDQASGHQATATVEVSI IESTWVSLEPIHLAE
NLKVLYPHMAQVHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN
SHGEDYAAPLELHVLVMENDNVPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSH
V VYQLLSPEPEDGV EGRAFQVDPTSGSVTLGVPLRAGQNILLVLAMDIAGAEGGFSSTCE
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTAIDADLEPAFRLMDFAIERGDTE
GTFGLDWEPDSGHVRLRLCKNLSYEAPSHEVVVVVQSVAKLVGPGPGATATVTVLVERV
MPPP KLDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVN DSEGWL CIEKFSGEVHTA
QSLQGAQPGDTYTVLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
TLGP NPTVQR DWRLQ TLNGSHAYLT LALHWV EPREHII PVVVSHNAQM WQLLVRVIVCRCNV
EGQCMRKVGRMKGMPTKLSAVGILVGTLVAIGIFLILIFT HWTMSRKKDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGAC**ATG**AGGTGGATACTGTTATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCAA
 GAAAAATTTTGGGGACCAAGTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAATTGAAGCTCAATTCTGGAATCTCCCTCCT
 TCAATCGGCCTGTGGATGTCCTGGTCCCCTGTCAGTCTGCAGGCATTAAATCCTTCCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTAGACAATGA
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTCAACTACGGGG
 CTTACCATTCCCTGGAAGCTATTACACGAGATGGACAACTTGCAGACTTCCCTGAC
 CTGGCGAGGGAGGGTGAAGATTGGACATTGTTGAAAACCGGCCATGTATGTACTGAAGTT
 CAGCACTGGAAAGGCCTGAGGCCTGGCGCCGTTGGCTGAATGCAGGCATCCATTCCCGAG
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
 GATCCAGCTATCACCTCCATCTGGAGAAAATGGATATTCTTGTGCTGTGGCAAATCC
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCCTCCGAAATC
 CTGGAAAGCTCCTGCATTGGTCTGACCCAAATAGAAAATCTGAAACGCTAGTTGCAGGAAAG
 GGAGCCAGCGACAACCCTTGCTCCGAAGTGTACCATGGACCCCACGCCAATTGGAAGTGG
 GGTGAAATCAGTGGTAGATTTCATCCAAAACATGGGAATTCAAGGGCTTCATGCACCTGC
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAGGCCAGATGCC
 GAGGAACCTGACAAGGTGGCGAGGCTGCGGCCAAAGCTCTGGCTCTGTGTCGGCACTGA
 GTACCAAGTGGTCCCACCTGCACCACTGTCTATCCAGCTAGCAGGGAGCAGCATGCACTGG
 CGTATGACAACGGCATCAAATTGCATTCACATTGAGTTGAGAGATACCGGGACCTATGGC
 TTCCCTCTGCCAGCTAACCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTAC**TAG**GCGATGGCTGCTCTGTCTACATTAT
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTTTCTACCTGTGAG
 TCAGAGCCCTCTGGTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGCTCTGGCGGTGCCCCCTGCAAGAACTGTTCTGCCAGCCTGCTCAATTGGTCTG
 CTGTTTTGATGAGCCTTTGTCTGTTCTCCTCCACCTGCTGGCTGGCGCTGCACTC
 AGCATCACCCCTTCTGGTGGCATGTCCTCTACCTCATTAGAACAAAGAACATC
 TGAGATGATTCTCTACCCCTACCCACATCTAGCCAAGCAGTGCACCTGCTCTGGTGGCACT
 GTGGGAGACACCACTGTCTTAGGTGGCTCAAAGATGATGAGAACATTCTGTAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCTCTGTTTTGGAGACAGAGTTTGCTCTGGTCTGCTCTGGTGGCACT
 CAGGCTGGAGTGTGATGGCTCGATCTGGCTCACACACCTCTGCCTCTGGTTCAAGCA
 ATTCTCCTGCCTCAGCCTTGTAGTAGCTGGTTTATAGGCGCATGCCACCATGCCTGGCTA
 ATTTGTGTTTTAGTAGAGACAGGGTTCTCCATGTTGGCTAGGCTGGCTCAAACACTCCA
 ACCTCAGGTGATCTGCCCTCCTGGCTCCCTTGTAGGCTGAATACAAAGTAGAGATCACTTCTTCAC
 TGCCGGGCCGTCCCCCTCTTGTAGGCTGAATACAAAGTAGAGATCACTTCTTCAC
 TGTGCTGAGAATTCTAGATACTACAGTTACTCCTCTTGTGTTTGTGTTTGTGTT
 ACCAGGATGGCGGGAGGGATCTGTGCACTGTAGGTACTGTGCCAGGAAGGCTGGTGAA
 GTGACCACATCAAATTGCAAGGATGGTGAATTATCCCCATCTGCTTAATGGGCTTACCTCCT
 CTTGCTCTTGTGAACTCACCTCAAAGATCTAGGCCTCATCTTACAGGTCTAAATCACTCAT
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCATTGTGCTGTGGTGTATCCTGTGTT
 TCCTTGTCTGGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTT
 TCTGTCTATTGTATCCTGGACCAAGTCTTAAGTAGAGCAAGAACATTCAACAGCT
 GCCTCTGTTCTACCTCACCTCAGCACGTACCATCTGCTCTTGTGTTGTGTT
 TTGTTTTGCTTTACCAAACATGTCTGAAATCTTAACCTCCTGCCTAGGATTGTACA
 GCATCTGGTGTGCTTATAAGCCAATAATATTCAATGTGAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSIQAFKSFLRSQGLEYAVTIEDLQALLDNEDEMHQHNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKVRRPAWVLNAGIHSREWI
SQATAIW TARKIVSDYQRDPAIT SILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQI IPTAEEETWLGLKTIMEHVRDNLY

Signal peptide:

amino acids 1-16

FIGURE 135

FIGURE 136

MASYLYGVLFAGVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVSLNTDFAFRLYRRLVLE
TPSQNIFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELOLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGK
VVDDIQQLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDAVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

FIGURE 137

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGC
 CTGAGTCCAAGATTCTCCAGGAACACAAACGTAGGAGACCCACGCTCTGGAAGCACCAG
 CCTTATCTCTCACCTCAAGTCCCCTTCTCAAGAACATCCTGTTCTTGCCTCTAAAG
 TCTTGGTACATCTAGGACCCAGGCATCTTGCTTCCAGGCCACAAAGAGACAG**ATGA**AGATGC
 AGAAAGGAAATGTTCTCCTATGTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCC
 AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC
 CACCAACTCTGGTCCAGTGTGACCTCCAGTGGGTCAAGCACAGCCACCATCTCAGGGTCCA
 GCGTGACCTCCAATGGGTCAAGCATAGTCACCAACTCTGAGTCCATACAACCTCCAGTGGG
 ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA
 CTCTGAGTCCAGCACAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC
 CCTCCAGTGGGCCAGCACAGTCACCAACTCTGGTCCAGTGTGACCTCCAGTGGAGCCAGC
 ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA
 GTCTAGCACACTCTCCAGTGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAAACCTCCA
 GTGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACACACTCCAGTGGGCCAGCACAGCC
 ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG
 CACAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACGACCTCCAATGGG
 CTGGCACAGCCACCAACTCTGAGTCCAGCACGACACTCCAGTGGGCCAGCACAGCCACCAAC
 TCTGACTCCAGCACAGTGTCCAGTGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGAC
 CTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACACTCCAGTGGGCTAGCA
 CAGCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAG
 TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTCCAG
 TGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGCCAACACAGCCA
 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGCCAGCACTGCCACCAACTCTGAGTCCAGC
 ACAACCTCCAGTGGGTAGCACAGCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGG
 TAGCACAGCCACCAACTCTGACTCCAGCACACACTCCAGTGTGAGGCCAGCACAGCCACCAACT
 CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAA
 TCCAGTGGGCCAACACAGCCACCAACTCTGGTCCAGTGTGACCTCTGCAGGCTCTGGAAC
 AGCAGCTCTGACTGGAATGCACACAACCTCCATAGTCATCTACTGCAGTGAGTGAGGCAA
 AGCCTGGTGGTCCCTGGTGGCGTGGAAATCTTCCATCATCACCCCTGGTCTCGGTTGTGGCG
 GCCGTGGGCTTTGCTGGCTCTTCTGTGAGAAACAGCCTGTCCCTGAGAAACAC
 CTTAACACAGCTGTCTACCACCTCATGGCCTCAACCCTGGCCTGGTCCAGGCCCTGGAG
 GGAATCATGGAGCCCCCAGGCCAGGTGGAGTCCTAACTGGTTCTGGAGGAGACAGTA
 TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCC**TGA**GCAGCCCCGGAAAGCAAG
 TGCCGCATTCTCAGGAAGGAAGAGACCTGGCACCCAGACCTGGTTCTTCATTCTAC
 CCAGGAGACCCCTCCAGCTTGTGAGATCTGAAAATCTGAGAAGGTATTCTCACC
 TTTCTGCCTTACAGACACTGGAAGAGAAATACTATATTGCTCATTAGCTAAGAAATAA
 ATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTGCCCCGGGTGGTATCTAG
 CTCTGAGATGAACTCAGTTAGGAGAAAACCTCCATGCTGGACTCCATCTGGCATTCAAAA
 TCTCCACAGTAAACCAAGACCTCAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 138

MKMQKGNVLLMFGLLHLEATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGSSVTSGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESTPSSGASTVTNGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSTS TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSESSTTSSGASTATNDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSESSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNDSSTSSEASTATNSESSTVSSGISTVTNSESSTTSSGANTATNGSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP GPGGNHGAPHRPRWSPNWFWRPVSSIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTCCCTGGCTCCTCTGCATCCTCCGACCTTC
CCAGCAATATGCATCTGCACGTCTGGTCGGCTCCTGCTCCCTCCTCTGCTACTGGGGGCC
CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGCAAGGCCCTGGATGGCATCAACAGTGGAAATCACGC
ATGCCGGAAGGGAAAGTGGAGAAGGTTTCAACGGACTTAGCAACATGGGAGGCCACACCGGC
AAGGAGTTGGACAAAGCGTCCAGGGCTCAACCACGGCATGGACAAGGTTGCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGTCAACAAACG
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTCCACACTGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAAACTTGGCCAAGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
TGCAGAATGCTCATAATGGGTCAACCAAGCCAGCAAGGAGGCCAACAGCTGCTGAATGGC
AACCATCAAAGCGGATCTCCAGCCATCAAGGAGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCCTTCATCAACCTTCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCTAAACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGAC
ATGACCTGGAGGGTTGGGGTGGGGACAGGTTCTGAAATCCCTGAAGGGGGTTGTACTG
GGATTTGTGAATAAACTTGATACACCA

FIGURE 140

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLQGVNHAADQAGKEVEKLQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

FIGURE 141

CTCCGGGTCCCCAGGGGCTGCGCCGGCGGCTGGCAAGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
 CCCGGGGGGCGATGACCGTGCCTGACCCCTGACTCACTCCAGTCCGGAGGGGGCCCCGGGGCAGACTCG
 GGGCGGACCGCGGGCGAGCTGCCGCCGTGAGTCCGGCGAGCCACCTGAGCCCAGGCCGGACACCGTC
 GCTCTGCTCTCCGA**ATG**CTGCGCACCGCGATGGGCTGAGGAGCTGGCTCGCCGCCCCATGGGCGCGCTGCCG
 CCTCGGCCACCGCTGCTGCTCTGCTGCTGCTCTGCTGAGCCGCCCTCCGACCTGGCGCTCAGC
 CCCGGATCACCTCTGGGCTCTGAAGAGCGGCCATTCCCTAGATTGAAGCTGAACACATCTCAAAC
 ACAGCCCTCTGCTGAGCAGGGATGGCAGGACCTGTACGGTGTGAGAGGCCCTTTGACTCAGTAGC
 AACCTAGCTCCTGCCAGCGGGAGTACCAAGGAGCTGCTTGGGTGAGACGAGAAGAAACAGCAGTC
 AGCTCAAGGCAAGGACCCACAGCGCAGTGTAAAACATCAAGATCCTCTGCCGTCAGCGCAGTC
 CTGTCACCTGTGGCACAGCAGCTCAGCCCCATGTGACCTACATCAACATGGAGAACCTCACCTGGCAAGG
 GAGAGAAGGGGAATGCTCTCTGAAGATGGCAAGGGCGTTGTCCTTCGACCCGAATTCAAGTCCACTGCC
 CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTCCAAGGGAATGACCCGCCATCTCGCGGAGC
 CAAAGCCTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTGTGGCCTCAGCCTAC
 ATTCTGAGAGCCTGGGAGCTTGCAAGGAGTGTGACAAGATCTACTTTTCTTCAGCAGACTGCCAGGAA
 TTTGAGTTTTGAGAACACCATTGTGTCGGCATTGCCGCATCTGCAAGGGGATGAGGGTGGAGAGCGGGTG
 CTACAGCAGCGCTGGACCTCTCAAGGCCAGCTGCTGTGCTCACGCCAGATGGCTTCCCTCAAC
 GTGCTGCAGGATGTCTCACGCTGAGCCCAGCCCCAGGACTGGCGTGAACCCCTTCTATGGGCTTCTCACT
 TCCAGTGGCACAGGGAACTACAGAAGGCTGCGCTGTGCTCACAATGAAGGATGTGAGAGAGTCTC
 AGCGGCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCGGTGCCACACCCGG
 CCTGGAGCGTGCATCACCAACAGTGCCTGGAAAGGAAGATCAACTCATCCCTGAGCTCCAGACCGCGTGTG
 AACTCCTCAAGGACCACTCTGATGGACGGGAGGTCCGAAGCCGATGCTGCTGAGCCACAGGCTCGC
 TACAGCGCGTGGCTGTACCCGCTCCCTGGCTGACACACCTACGATGTCCTTCTGGTACATGGGACTGGTAC
 GGCGGCTCCACAAGGAGCTGAGCGTGGGGGGGTGACATCATTGAGGAGCTGAGATCTTCTCATGGGA
 CACCCGTGAGAATCTGCTCTGGACACCCACAGGGGGTGCTGTATGGCCCTCACACTGGGCTAGTCCAG
 GTGCCCATGGGCAACTGCAAGCACGTGACCTCTACAGCCTCAGCTGGCCACCAGGGGTGGATCCAGGACATGAG
 AGCGGCTCCAGCTGCAAGCACGTGACCTCTACAGCCTCAGCTGGCCACCAGGGGTGGATCCAGGACATGAG
 GGAGCCAGGCCAAGGACCTTGCAGCGCTTCTGGTTGTGCCCCGTCTTGTACCAACAGGGAGAACCA
 TGTGAGCAAGTCCAGTCCAGCCAAACAGTGAACACTTGGCTGCCCTCCTCTAACCTGGGACCCGA
 CTCGGCTACGCAACGGGCCCCCTCAATGCCCTGCCCTGCCACGTGCTACCCACTGGGACCTGCTGCTG
 GTGGGCAACCAACAGCTGGGGAGTTCCAGTGGTCACTAGAGGAGGGCTCCAGCAGTGGTAGCCAGCTAC
 TGCCAGAGGTGGTGGAGGACGGGTGGAGACACAGATGAGGGTGGCAGTGTACCCGTATTATCAGCACA
 TCGCGTGTGAGTGCACCAAGCTGGTGCAAGGCCAGTGGGTGCAAGACAGGTCTACTGGAAGGAGTCTGGT
 ATGTGCACGCTTTGTGCTGGCCGTGCTCCCAGTTTATTCTGCTTACCGCACCGAACAGCATGAAA
 GTCTCTGAAGCAGGGGAATGTGCCAGCGTGCACCCCAAGACCTGCCCTGTTGCTGCCCTGAGACCCGC
 CCACTCAACGCCCTAGGGCCCCCTAGCACCCCGCTGATCACCGAGGGTACAGTCCCTGTCAGACAGCCCCCG
 GGGCCCGAGTCTCACTGAGTCAAGAACAGGCCACTCAGCATCCAAGACAGCTCGTGGAGGTATCCCAGTG
 TGCCCCCGGCCCGGGTCCGCTGGAGATCCGTACTCTGGTGT**GA**AGAGCTGACTTCCAGAGGACGC
 TGCCCTGGCTTCAGGGGTGTGAATGCTGGAGAGGGTAACCTGGACCTCCCGCTCTGCTTCTGTGGAAAC
 ACGACCGTGGTGGCCGGGCTTGGGAGGCCCTGGAGCCAGCTGGCTGCTCTCCAGTCAGTAGCGAAGCTCC
 TACCAACCGACACCCAAACAGCCCTGGCCCCAGAGGTCTGCCAAATATGGGGCCTGCTAGTTGGTGGAA
 CAGTGTCTTATGTAACAGGCTTGTAAAAAAACATTCACATGGGCTCCAGGGTGTGGGAGTGCATCAAAGTGG
 ATAGCATGGCATGCAAGCACACAGCGCTGCTCCAGTTCATGGCTCCAGGGTGTGGGAGTGCATCAAAGTGG
 TTGTCTGAGACAGAGTTGAAACCCCTACCAACTGGCCTCTTACCTCCACATTATCCCCTGCAACCGGGCTG
 CCTGTCTCACTGCAAGATTGAGGACAGCTTGGCTGCGTTGCTGCTTGCAGTCAGCCAGGATGTAGTTG
 TTGCTGCCGTGCTCCCACCACTCAGGGACCAAGAGGCTAGGTGGCAGTGCAGGCCCTCACAGGTCTGGGCTC
 GGACCCAACCTCTGGACCTTCCAGCCTGATCAGGCTGTGGCCACACGAGAGGACAGCGCAGCTCAGGAGAGA
 TTTCTGACAATGTACGCCCTCCCTCAGAATTGAGGAGAGACTGTGCGCTGCCCTCCGTTGCGTGA
 GAACCCGTGTGCCCTCCACCATATCCACCCCTGCTCCATTTGAACTCAAACACGAGGAACTAACGTGACC
 CTGGCTCTCCCCAGTCCCCAGTTCAACCTCCATCCCTCACCTCCTCAACTCTAAGGGATATCAACACTGCC
 AGCACAGGGGCCCTGAATTATGTTTATACATTAAAGATGCACTTATGTCATTTTAATAAAA
 GTCTGAAGAATTACTGTTAAAAAAAAAAAAA

FIGURE 142

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPLL LLLLQPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLLSRDGR TL YVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRC P
FDPNFKSTALVVDGELYTGTVSSFQGNDPAISRSQSLRPTKTTESSLNLQDPAFVASAYIPE
SLGSLQGDDD KIYFFFSETGQEFEFFENTIVSRIARI C KGDEGGERVLQQRWTSFLKAQLLC
SRPDDGF PNVLQDVFTLSPSPQDWRTLFYGVFTSQWHRGTTEGSACVFTMKDVRV FSG
LYKEVNRETQQWYT VTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGR LHKA VSVGPRVHII EELQIFSSGQ
PVQNLLLDTHR GLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVS LYQP
QLATRPWI QDIEGASA KDLCSASSV VSPSFVPTGEKPCEQVQFQ PNTVNTLACPLLSNLATR
LWL RNGAPVN ASASCHVLPTG DLLL VGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPII I STSRV SAPAGG KASWGADRSY WKEFLVMCTLFVLA VLLPVL FLLYRHRNSM
KVFLKQGECA SVHPK TCPVVL PPETRPLNGLGPPSTLDHRGYQSLSDSPPGARVFT ESEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGGCGGCCGCGCAGGGCTACGAAGAGGACGGGGACAGGCCTGCGAACCGA
GCCCAAGCCAGCGGAGGACGCCGGCAGGGGGACGGGACTCGCTGCCGCCGCTGCCGCGCTGCCGCG
TGCCGGCCCCGCGTCCCCGCGCGAGCGGGAGGGAGCCACCTCGCGCCGAGCGCCGCTAGCGCGCG
CGGGCATGGTCCCCCTTAAAGGCGCAGGCCGCCGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
CCTGCGGCGGCTGGGGGCCGATGGCGCGGGGCCCGCGCGCGCGCTGCCGGGGCTCGCCGGGGCTCG
CGCGCTAGGGCGGGCTGGCTCCGTGGCGGGGAGCGGGCTGAGGGCGCGAGCGCTGCCGGCGCG
GGCGCGGGCGGCCGG
ATGCGCCG
TGCTCGGGCTCGTCTGGCTCGTGGCTCGCGCTCGTCCCTGCCCGGGCTCCGAGCTGAAGCGAGCG
GCCCACGGCGCCGCCAGCCCCGAGGGCTGCCGGTCCGGCAGGCCGGCTTCCAGGCCGGGGCGCG
GCGATGCGCGCGGGCGCAGCTCTGCCGCCGGCTCGACCCAGATGCCGCCGCCGCGACAGGAACTTCTCT
TCGTGGAGTCATGACGCCAGAAATACTGCAGACTCGGGCGTGGCCGCTACAGAACATGGTCAAAGACAA
TTCTGGAAAGTTCAAGTCTCAAGTGAGGGTCTGACACATCGTACCAATTCAAGTAGTGCCACTACGGG
GTGTGGACACTCTACCCGCCAGAAGAAGTCTCATGATGCTCAAGTACATGCACGACCAACTTGGACA
AGTATGAATGGTTATGAGAGCAGATGATGACGTACATCAAAGGAGACCGCTGAGAAACTCTGAGGAGTT
TGAACAGCAGCGAGCCCTCTTCTTGGCAGACAGGCCTGGCACCGAAGAAATGGGAAACTGCCCTGG
AGCCTGGTGAAGAACTTCTGCATGGGGGGCTGGCGTGAATCATGAGCCGGAGGTGCTCGGAGAATGGTGC
ACATTGCGCAAGTGTCTCCGGAGATGTACACCACCATGAGGACGTGGAGGTGGAGGCTGTGCGAGGTTTG
CAGGGGTGAGGTGTCTGGTCTATGAGATGCCAGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
ACATTAGAGATCTCCATAACAGTAAAATTCCAAGCTACATACACCCCAACAAAAACCCACCTACCAAGT
ACAGGCTCCACAGCTACATGCTGAGGCCAGAATATCGAGCTCCGCCATCGCACAAATACAGCTGCACCG
TTGCTCTGATGAGCAAATACAGCAACACAGAAAATTCTAAAGAGGACCTCCAGCTGGAAATCCCTCTTCA
TGAGGTTTCAAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGAGTTCTGACTGGAAAATACTGTATT
TTGACGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGAGGGAGCCTGGACACATTGTCATGCAG
TGGAGATGATCAATGCCAACGCCAGACAGAGGGCGCATATTGACTTCAAGAGATCCAGTACGGCTACCG
GGGTGAAACCCATGATGGGCTGAGTACATCTGGACCTGCTCTGTACAAAAGACAAAGGGAAAGAAA
TGACGGTCCCTGTGAGGAGGCACCGTATTACAGCAGACTTICAGCAAAATCCAGTTGTGGAGCATGAG
TGGATGACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCTTCTCTCTCAAACACTCCCTGAAGA
AGCTCGCCCTTCAAGCTCCCTGGGTCGAAGAGTGAACAGCACAAAGAACCAAAGATAAAAGATAAC
TTCCCTTGTCTGGGCTTCGACATGTTGTGAGATTATGGGAAACTTGTAGAAGACGTGTCTTAT
CCCCAATCAGACCTCAAGCTCGTGGTTCTGTTCAATTCTGACTCCAACCTGACAAGGCCAACAGT
GAGATTACCGCATTAAAGTACCTAAAGCCGACATGCGAGATTGCGCTGTCAGGAGGTTCAAGAG
GCCCTGGAAAGTAGGATCCTCCCAGTTAACATGAATCTTGTCTTCTGCGACGCTGACCTCGTGT
CAGAACATTCTCAGCGATGTCGAGCAAATACAGTCTGGGCCAACAAATATATTCTCAATCAT
CTCAGCCAGTATGACCCAAAGATTGTTATAGTGGAAAGTCCAGTGACAACCATTTGCCCTTA
ACTCAGAAAATGGCTCTTCTGAGGAGATCTTGTCCAGTGAGGAGTTGAGCTGGCTTGATGTT
GGAGAAACTATGGTTTGCGATCACGTGATTATAAGGGAGATCTTGTCCAGTGAGGAGTT
TCCAAGGCTGGGGCTGGAGGATGTGGACCTTCAACAAGGTTGTCAGGCCAGTTGAAGAC
AGGAAGTAGGAGTAGTCCACGTCACCATCTGTCTTGTGATCCAATCTTGACCCAAACAGT
ACAAAATGTGCTGGGGTCCAAAGCATCGACCTATGGTCCACCCAGCAGCTGGCTGAGAT
GTGGGAAAGACTATGGCTCTGAGGAGACAGCCTAATGCGCTTCTGAGGAGCTTGTGAG
GTTACAGTAAAGCAGCAATAATAATGGCTCAGTGAGGAGACAGCCTAATGCGCT
TAATTATCTAATTATTTCAAAAATTGTTGATGATCAGTTTGAGTCCGTATACAAG
GAGATTGTTTCTTACATAGGACTCTTAAAGATTGAGCTTCTGAAACAAGAAG
GTGATCAGTGTGTTGCTTGTGAAACATCTTCTGAGGAGATGTGAA
CACATCTCTGCTGAACATTATGAGCAGACCTGCTTAACTTGTGACTGAA
TTTAAAAAAATGTTCTTGTGAGACCTTGTCTCAGTCTATGGCAGAAA
ACTGTAACATTCTGCTTGTGTTGTTGTTGTTGAGACGGAGTCT
TATTGTAACAAAACACTGTAACTCTGGTAAATGTTCTGTTGATTGTT
GTTTGTTTTTTTACAATTGTTAAAGCCTTCACTGTTGAGGAGT
GCTGTTCATATTGCTTCAAGGAGACCTTCCAGAGTGTGAT
CACGTTCTCATGTTGACTCTGCTCAGCATGG
CACGTAGGTTTTGTTGTTGTTGTTGTTGAGACGGAGTCT
CAGTGGCGCAATCTGGCTCACTTAACTCCACTCCCTGGTCAAG
CAATTCCCTGCCCTGCTTGCCTCCCGAGT
AGCTGGGATTACAGGACACACCACGCCAGNTAGTT
GCAAGGCCAGCTGGCCACGTAGGTTAAAGCAAGGGCGTGAAGAAG
GGCACAGTGAGGATGTGGCTGTT
TGGTAGTTCTATTGGCCTAAATAGACCTGGCATTAAATT
CTAAGAAGGATTGGCATTTCCTCTTCTGACCC
CTCTTAAAGGGAAAATATTAAATGTTAGAATGACAAAG
GATGAATTATTACAATAATCTGATGTACACAGACT
GAAACATACACACATACACCC
TAATCAGGTTGGGGAAAATGTATT
TGTTGTTGTTGTTCTCATCTGCTG
TGTTATGTGGGTTGAGATGGTTTCACTTCT
TTTAAATCTGTTGTTAGAGCTGCCATT
CTTGAGTACCTGTAGTTAGTATT
TATGTGTATCGG
GAGTGTGTTAGTGTGTTATTGCA
GATCTCCAAAGATTT
CTGTTGAAACGCTTT
CCCCCTCC

FIGURE 143B

TTAATTTTATATTCTTACTGTTACTAAATATTAAGTGTCTTGACAATTGGTGCATGTGTTGG
GACAAAAGTGAATGAATCTGTCATTATACCAAGTAAATTCTCAGATCAAATGTGCCTAATAAATTGTT
TTCATTTAGATTCAAACAGTGATAGACTGCCATTTAACACGTCATTGGAGGGCTCGTATTGTAAATAG
CCTGATGCTCATGGAAAAATAACCAGTGAACAATATTTCTATTGACTTTGAACCATTGTCTCATT
ATTCCCTGTTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAACTAAACACGAAAAAA

FIGURE 144

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRRAWLSVLLGLVLGFVLASRLVLPRASELKAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDDPGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEG
SDTSVPPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDHLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDEIQLGIPPSFMRFQPRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPMYGAEYILDLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVPFQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVVLNFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESSLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPNDHFAFT
QKTGFWRNYGFGITCIYKGDLVRVGGFDVSIQGWGLEVDLFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQQIAEMWLEKNDPSYSKSSNNNGSVRTA
```

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGCAGGTACTCCGCTGACACCTTCCC
 TTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
 ACGGACGACGCCTATGAAAGCCCTTAGCCTCTAGTTGCGCTTTGCTATGGCCTCGTCTG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAAACTTGAATCATTATATA
 CAAGTTTAGAGAACCTAGTACGAAGTGTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAATC
 TAACTCTCCAAAACATGTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA
 CACATGGAGACGCTTCAACTGAGAATGATGTTTAACCAATCCTATCAGTGAAGAAACTACA
 ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCC
 ATTCTGGTCGATCAAACCAAACATGTTCCATTGTTGCATGCAGAGGAACCTTATATTG
 AAAATGAAGAGGCCAGGCCAGGCCAGGCCAGCTGCAAAACAAACTGAGGCACCAAGAATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC
 CACTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
 CAGGTGAAACTGCGATAGAAAAACCGAAGAGTTGGAAAGCACCCAGAGAGTTGGAATAAT
 GATGACATTTGAAAAAAATTTAGATATTAATTCAAGTGCAACAGGCACCTTCTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
 TTGCTCTAGCAGCAGCAGAACATAAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAAACTGTTATTAACATGCTGTGAATTC
 TAGATCTAAACTCTATGAATATTTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG
 CTGCTACAGTATTCAATAACATTAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTATTTAAACAATAATATAAAATTAAACCTACTTGATATTCCATAACAAAGCTGA
 TTTAAGCAAACGTGCTTTTACAGGAGAAATAATCATATTGCAATTCAAAAGTTGTAT
 AAAAATATTTCTATTGTTCAATGTGCCAACATCTTATGTGTATGTGTTATGAACA
 ATTTCATATGCACTAAAAACCTAATTAAAATTTGGTCAGGAAAAAA

FIGURE 146

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLNPISEETTFPTGGFTPEIGKKKTESTPFWSI
KPNNVSIVLHAEPYIENEPEPEPAAKQTEAPRMLPVVTESSSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFKGKHPEWNNDDILKKILDINSQQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAEEHKLKTMYKSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPREMREKAATVFNTLKNMCRSRRVTALLKVY
```

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCCCTGAGACAGCTGGCTG
 ACCTCCAAATCATCCATCCACCCCTGCTGTCACTGTTTCATAGTGTGAGATCAACCCACA
 GGAATATCC**ATG**GCTTTGTGCTCATTTGGTTCTCAGTTCTACAGACTGGTGTAGGACA
 GTGGCAAGTCACTGGACCGGGCAAGTTGTCCAGGCCTGGTGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTCTTCCTGAGACCAGTCAGAGGCTATGGAAGTGCAGGTTCTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGAAGACTGGGAATCTAACGCAGATGCCACA
 GTATCGAGGGAGAACTGAGTTGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTAAGGC
 TAAAAAACATCACTCCCTCGACATCGGCCTGTATGGGTGCTGGTCAGTCCCAGATTAC
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGCTCACTCCTCTCATTCCAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCCTGCCTCAGGCTGGTCCCCCAGC
 CCACAGCCAAGTGGAAAGGTCACAAGGACAGGATTGTCTCAGACTCCAGAGCAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCATTATAGTCAGGAAAATGCTGGAGCAT
 ATTGTGTTCCATCCACCTTGCTGAGCAGACTCATGAGGTGGAATCCAAGGTATTGATAGGAG
 AGACGTTTCCAGCCCTCACCTTGGCGCTGGCTCTATTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTCATGGGATGATAATTGTTCTCAAATCCAAGGGAAAATCCA
 GGCGGAACTGGACTGGAGAAGAACGACGGACAGGCAGAATTGAGAGACGCCCGGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCGAAGCTCTGCCTTGTATGAAA
 ACTGTAACCCATAGAAAAGCTCCCCAGGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAA
 GAGTGTGGTGGCTCTCAGGGTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGAC
 AAAATGTAGGGTGGTATGTGGAGTGTGTCGGGATGACGTAGACAGGGGAAGAACAAATGTG
 ACTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTCAC
 ATTCAATCCCCATTTATCAGCCTCCCCCCCAGCACCCCTCTACACGAGTAGGGTCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTCTTCAATAACAAATGACCAGTCCCTATTATACC
 CTGCTGACATGTCAGTTGAAGGTTGAGACCTATATCCAGCATGCGATGTATGACGA
 GGAAAAGGGACTCCATATTCAATGTCAGTGTCTGGGA**TGA**GACAGAGAACCCCTG
 CTTAAAGGGCCCCACACCACAGACACAGCCAAGGGAGGTGCTCCGACAGGTGGC
 CCCAGCTCCTCTCGGAGCTGCGCACAGAGACTCACGCCCTACTCTCCTTAGGGAGC
 TGAGGTTCTCTGCCCTGAGCCCTGAGCAGCAGCGAGTCAAGCTTCCAGATGAGGGGGAT
 TGGCCTGACCTGTGGGAGTCAGAACCCATGGCTGCCCTGAAGTGGGAGGAATAGACTCA
 CATTAGGTTAGTTGTGAAAATCCATCCAGCTAACGATCTTGAACAAAGTCACAACCTCC
 CAGGCTCCTCATTGCTAGTCAGGGACAGTGATTCCCTGCCCTCACAGGTGAAGATTAAAGAGA
 CAACGAATGTGAATCATGCTGCAGGTTGAGGGCACAGTGTGCTAATGATGTTTTA
 TATTATACATTTCCCACCAATAACTCTGTTGCTTATTCCACATTAATTACTTTCTCTA
 TACCAAATCACCATGGAATAGTTATTGAACACCTGCTTGTGAGGCTCAAAGAATAAAGAG
 GAGGTAGGATTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAAACCAGGCAAAG
 AAAACAGAAGAAGAGGAAGGAAAATCACAGGTCCATATCCCTCATTAACACAGACACAAAAAA
 TTCTAAATAAAATTAAACAAATTAAACTAAACATATTTAAAGATGATATATAACTACT
 CAGTGTGGTTGTCCCACAAATGCAGAGTTGGTTAATATTAAATATCAACCAAGTGTAAATT
 CAGCACATTAAAGTAAAAAGAAAACCATAAAAAAAAAAAAAAA

FIGURE 148

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAAL GSLPLISIVGYVDGGIQLLCLSSGWFPQOPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKV LIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGVYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHYFTFNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAAGAGTTGTTGGAACCTGGTTATCGGCCTCGTCATCTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTCATTATGTGAGATATAATCAAAGAACGACTACAA
 TTACTATAGCACATTGTCATTACAACGTGACAAACTATATGCTGAGTTGGCAGAGAGGCTT
 CTAACAATTTCAGAAATGAGCCAGAGACTTGAATCAATGGTAAAAATGCATTTATAAA
 TCTCCATTAAGGAAAGAATTGTCAAGTCTCAGGTTATCAAGTTCAACAGAACGATGG
 AGTGTGGCTCATATGCTGTTGATTGTAGATTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAAATTGTTCAACTGTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCTAAAGTA
 GATCCTCACTCAGTAAAATTAAAAAAATCAACAAGACAGAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAAACCTCTAGGTAGCAGTCAGGATCGTTGGTGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTACAACATATAA
 GAACCCGCCAGATGGACTGCTCCTTGGAGTAACAATAAACCTTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAATACAAACACCCATCACATGACTATGATATTCT
 CTTGCAGAGCTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTGTCTCCCTGA
 TGCAATCCTATGAGTTCAACCAGGTGATGTGATGTTGTGACAGGATTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGAECTCTGGAGGACCACTGGTTAGTCAGATGCTA
 GAGATATCTGGTACCTGCTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCCAACAAG
 CCTGGTGTAACTAGAGTTACGGCCTGCGGGACTGGATTACCTCAAAACTGGTATCTA
AGAGACAAAAGCCTCATGGAACAGATAAACATTTTTTGTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTGGAGAACAGACTTGCAAAACAGCTAGATTGACTGATCTCAATAAAC
 TGTTGCTTGATGCATGTATTTCTCCAGCTCTGTTCCGCACGTAAGCATTGCTTCTG
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTGAAACTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCAAGGTGAGAACACAAGGAGTGAAAGAAAATA
 TTGTTGACATAAATTGTAATGCATATACAAATTGAAGCACTCCTTCTCAGTTCTC
 AGCTCCTCTCATTCAAGAAATATCCATTTCAGGAGTGAGAACACAAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAAATCCCCTACATTATTGGCACAGAAAAGTATTAGGTGTTCTTAGT
 GGAATATTAGAAATGATCATATTCAAGGTCAAGCAAAGAACAGCAGAACATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAAGAACGCAAGATATA
 TCCTTATTTCTTCAAAACAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTGTG
 ACCTATAATAATTACAAACTCATGCAATGTAATTGTTCTAAGCAAATTAAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAACCCCA

FIGURE 150

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPHDYDISLAELOSSPVPTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDEAKPNKPGVYTRVTALRDWITSKTGI
```

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCAAACGGCATTGAAGTTGAAGATAAACCTGACAGCA
CAGCCTGAGATCTGGGGATCCCTCAGCCTAACACCCACAGACGTAGCTGGTGGATTCCCG
CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGCTCTCCCTGCCTTGTGGCTCCTGGC
CGTGACCTTCTGGTCCCAGAGCTAGCCCTGGCCCTCAAGACTTGAAGAAGAGGAGG
CAGATGAGACTGAGACGGCGTGGCCGCCCTTGCCGGCTGTCCCCCTGCGACTACGACCACTGC
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCCTGCCTGTGCC
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCCTATTGC
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCTCTCCCCGGCTCCACTACTGG
CTGCTGCTTGGGACGGCAGCGAGGCTGCGCAGAAGGGCCCCCGCTGAACGCTACGGTCC
CAGAGCCGAACTGAAGGGGCTGAAGCCAGGGGCTTATGTCGTTGCGTAGTGGCCGCTA
ACGAGGCCGGGCAAGCCGCGTGCCTCAGGCTGGAGGAGAGGGCCTCGAGGGGCCGACATC
CCTGCCTTCGGGCCTTGCAGCCGCCTTGCGGTGCCGCCAACCCCCGCACTCTGGTCCACGC
GGCGTCGGGTGGCACGCCCTGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
GCCTGCGCAGTCGCTGGGCTGCCCGCCGAGCCGCCGAGCCGCAGGGCGCTC**TGA**
AAGGGGCCTGGGGCATCTCGGGCACAGACAGCCCCACCTGGGCGCTCAGCCTGCCCG
GGAAAGAGGAAAACCGCTGCCCTCAGGGAGGGCTGGACGGCGAGCTGGAGGCCAGCCCCAG
GCTCCAGGGCCACGGCGAGTCATGGTCTCAGGACTGAGCGCTTGTAGGTCCGGTACTT
GGCGCTTGTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGCCCCAATTTTTTTTA
AGCGGCCAGATAATAATGTAACCTTGCGGTTAAAAAAAAAAAAAA

FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRHLQVPCKE
LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA
AQKGPPLNATVRRAELKGLKPGGIYVVCVVAANEAGASRVPQAGGEGLEGADI PAFGPCSRL
AVPPNPRTLVHAAVGVGTALALLSCAALVWHFCLRDRWGCPRRAAARAAGAL
```

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
CTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCAGGC GGCGTGGGCACCGGG
CCCAGCGCCGACGATCGCTGCCGTTGCCCTTGGGAGTAGGATGTGGTCAAAGGATGGGC
TTCTCCCTTACGGGCTCACA**AT****GGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT**
CTACGCCCTCAATCTGCTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTCTGCTTGG
TGAGGGACTACCTAAATAATGTTCTCACTTAAC TGAGAAACGAGGGTAGAGGAAGCAGTC
ATTTGACTTACTTCCGTGGTCATCCGGCATGATTGCTGTTGCTGTTCCATTATCAT
TGTGGGATGTAGGATATTGTGGAACGGTAAAAGAAATCTGTTGCTTGGACATATGAACAG
TTGGAAGTTGCTTGTCACTTCTGTAGAAGACTGGCTGTCGTTGGACATATGAACAG
GAACTTATGGTCCAGTACAATGGTCAGATATGGTCACTTGAAAGCCAGGATGACAAATT
TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAACTTTTCAAGAGAGAGTTAAGT
GCTGTGGAGTAGTATATTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCAGAT
TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCAAACAGGCCACCAGGAAGATCTCAGTGA
CCTTATCAAGAGGGTGTGGGAAGAAAATGTATTCCCTTTGAGAGGAACCAAACAAC
AGGTGCTGAGGTTCTGGGAATCTCATTGGGTGACACAAATCTGGCCATGATTCTCAC
ATTACTCTGCTCTGGCTCTGTATTATGATAGAAGGGAGCCTGGACAGACCAAATGATGTC
CTTGAAGAATGACAACCTCAGCACCTGTCACTGCCCTCAGTAGAACACTGTTGAAAC
TGTCAAGAATCTTGAACACACATGGCAAACAGCTTAATACACACTTGAGATGGAG
GAGTT**TAA**AAAGAAATGTACAGAAGAAAACCACAAACTTGTGTTATTGGACTTGTGAATT
TTTGAGTACATACTATGTGTTCAGAAATATGTAGAAATAAAATGTTGCCATAAAATAACA
CCTAACGATATACTATTCTATGCTTAAATGAGGATGGAAAAGTTCATGTCATAAGTCAC
CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
CTGTGTATGACTTTACTGAACACAGTTATGTTGAGGCAGCATGGTTGATTAGCATTT
CGCATCCATGCAAACGAGTCACATATGGTGGACTGGAGCCATAGTAAAGGTGATTACTT
CTACCAAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATA
ACTTTTATTACTCAGCGATCTATTCTGATGCTAAATAATTATATATCAGAAAAC
AATATTGGTACTACCTAAATGTGATTGGTCTGGTTACTAAAATATTCTACCACTAAAA
GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTGGTATATAAGTCTGTAAA
TCTGTATAATTAGCATCATTATTTAGCCTTCCTGTTAATAAAGCTTACTATTCTGT
CCTGGCTTATATTACACATATAACTGTTATTAAATACTAACCAACTAATTGAAAATT
CCAGTGTGATACATAGGAATCATTATTAGCAAGTGTAGTCTGGTCTTAGGAAGTTAA
GAAAATTGACACATAACTTAGTGTGATTAGCAAGGACTTGTATGCTGTTCTCCAAATG
AAGACTCTTTGACACTAACACTTTAAAGCTTATCTTGCCCTCTCCAAACAAAGAA
GCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTCTTTCTCCAGAAAAT
GCTTGTGAGAATCATTAAACATGTGACAATTAGAGATTCTTGTGTTATTCACTGATTA
ATATACTGTGGCAAATTACACAGATTATAAATTGTTACAAGAGTATAGTATATT
GAAATGGGAAAAGTGCATTACTGTATTGTTATTCTCAGAATATGGAA
AGAAATTAAATGTGTCATAAAATTCTAGAGAGTAA

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMWDPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRLFGISIGVTQILAMILTITLLWAL
YYDRREPGBTDQMMSIKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTGCTCAGCGGACAAGGATGCTGGCGTGAGGGACCAAGGCCTGCC
 TGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTGGGGTACAAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGC**ATG**TACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGAAACCCGTATCCCCATGGAGACCTCAGAAAGGTGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGCCTCATCAAGG
 TGATTCTGGATAAATACTACTTCCTCTGCAGGGCAGCCTCTCCACTTCATCCGAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGAACTGGTTCTGCCTGTTGACAACACTCACAGAACGCTCTGCTGAG
 ACAGCCTGTAGGCAGATGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAAGGAGATCTGGA
 TGGTGTGAAATCACAGAAAACAGCCAGGAGCTCGATCGGAACACTCAAGTGGCCCTGTC
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTGCCTGTGGGAAGAGCCTGAAGACCCCCGT
 GTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTACGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATTGGACCCCCACTGGGCCTCACGGCAGCCCAC
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCCAGGCTCAGACAAACTGGC
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCATGTACCCAA
 AGACAATGACATGCCCTCATGAAGCTGCAGTCCCACACTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTTGATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATTGGA
 TGGGGCTTACGAAGCAGAATGGAGGGAAAGATGTCTGACATACTGCTGCAGCGTCAGTCCA
 GGTCAATTGACAGCACCGGTGCAATGCAGACGATGCGTACCAAGGGGAAGTCACCGAGAAGA
 TGATGTGTGCAGGCATCCCGGAAGGGGTGTGGACACCTGCCAGGGTACAGTGGTGGGCC
 CTGATGTACCAATCTGACCAAGTGGCATGTGGGGCATCGTTAGCTGGGCTATGGCTGC
 GGGCCGAGCACCCAGGGAGTACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCTTGCACTGCTGGAGCCGCTCCTCCTG
 CCCTGCCACCTGGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTGGTACACCC
 CTCTGCCACAGCCTCAGCATTCTGGAGCAGCAAAGGGCTCAATTCTGTAAGAGACCC
 TCGCAGCCCAGAGCGCCCAGAGGAAGTCAGCAGCCTAGCTCGGCCACACTTGGTGC
 AGCATCCCAGGGAGAGACACAGCCCACCTGAACAAGGTCTCAGGGTATTGCTAAGCCAAGAA
 GGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTGAAAAGCCAGATCACTGTGG
 CTGGAGAGGAGAAGGAAAGGGTCTGCCAGCCCTGTCCGTCTCACCCATCCCCAAGC
 TAATAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCACTGTGGTATGACTACCG
 TTACCTACTGTTGTCATTGTTATTACAGCTATGCCACTATTATAAGAGCTGTAA
 CATCTCTGGCAAAAAAA

FIGURE 156

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYF
LCGQPLHFI PRKQLCDGEELDCPLGEDEEHCVKSFP EGPAVAVRLSKDRSTLQV LDSATGNWF
SACFDNFTEAL AETACRQM GYSRAVEIGPDQ DLDV VEITEN SQEL RMRN SSGP CLSGSLVSL
HCLACGKSLKT PRVVG GEEAS VDSWP WQVSI QYDK QHVC GGSIL DPHW VLTA AHCF RKHT DV
FNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGT VRPICL PFFD
EEILT PATPLI IIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDT CQGD SGGPL MYQSDQ WHVVGIV SWGY GCGGP STPGV YTKVSAYLN WIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCAGTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGCATCCCCAGGCTCCAG
 AGCTCCCTGGTGACAGTGTGGCTGAGC**ATG**GCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCC
 TTTCCCTCTCCAAGTGCCTCAGCTGCTGCCGACGACCGGGGGAGGCAGGGCCATGCCA
 GGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCCACCAGAACGGGCTCCAGGATTTGACA
 CTCTGCTCCTGAGTGGTATGGAAATACTCTACGTGGGGCTCGAGAACGCATTCTGCCCTGGATATCCAGG
 ATCCAGGGGTCCCAGGCTAAAGAACATGATAACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCCTTA
 AGAAGAACAGCAATGAGACACAGTGTTCAACTTCATCCGTGCTTGTTCTAACATGTCACCCATCTACAC
 CCTGCGGCACCTTCGCCTCAGCCCTGCTTGACTCTCATGAACTCAAGATTCCACCTGTTGCCATCTCGG
 AGGACAAGGTATGGAGGGAAAAGGCCAAAGCCCCTTGACCCGCTCACAAAGCATACGGCTGTCTGGTGGATG
 GGATGCTCTATTCTGGTACTATGAACAACTCCTGGCAGTGAGCCATCCTGATGCGCACACTGGATCCCAGC
 CTGCTCTCAAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCCTTGTGGCAGGCATCCCTCGACCC
 AGGTCGTCTACTTCTTCGAGGAGACAGCCAGCGAGTTGACTTCTTGAGAGGCTCCACACATCGGGGTGG
 CTAGAGTCTGCAAGAACATGACGTGGCGGGCAAAGCTGCTGCAGAAGAACAGTGGACCACCTCCTGAAGGCCAGC
 TGCTCTGCACCCAGCCGGGGCAGCTGCCCTCAACGTATCCGCCACCGGGCTCTGCTCCCCGCCATTCTCCA
 CAGCTCCCCACATCTACCGAGTCTCACCTCCAGTGGCAGGTTGGCGGGACCAGGAGCTGCGGTTGTGCCT
 TCTCTCTTGGACATTGAACGTGTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACCTCACGCTGGACTA
 CTTATAGGGCCCTGAGACCAACCCCCGCCAGGCAGTTGCTCAGTGGCCCTCCTGATAAGGCCCTGACCT
 TCATGAAGGACCATTCTGATGGATGAGCAAGTGGTGGGACGCCCTGCTGGTAAATCTGGCTGGAGTATA
 CACGGCTGCACTGGAGACAGCCAGGGCTTGATGGCACAGCCATCTGTATGTACCTGGAACACCACAG
 GGTCGCTCCACAAGGCTGTTAAGTGGGACAGCAGTGCTCATCTGGTGAAGAGATTGAGCTGTTCCCTGACC
 CTGAACCTGTTGCAACCTGCACTGGCCCCACCCAGGGTGCAGTGTTGAGGCTCTCAGGAGGTGTCTGG
 GGGTCCCCGAGCCAAGTGTAGTGTCTATGAGAGCTGTTGACTGTGCTTGGGACCCCCACTGTGCCT
 GGGACCCCTGAGTCCGAACCTGTCCTGTCGCCCCAACCTGAACCTGGAAAGCAGGACATGGAGCGGG
 GGAACCCAGAGTGGCATGTGCCAGTGGCCCATGAGCAGGAGCCTCGGCCTCAGAGGCCCGCAAATCATTA
 AAGAACGTCTGGCTGCCCCAACTCCATCCTGGAGCTCCCTGCCCTACCTGTCAGCCTGGCTCTTATTATT
 GGAGTCATGGCCAGCAGCAGTCCCAGAACGCCTTCCACTGTCTACAATGGCTCCCTTGCTGATAGTGCAGG
 ATGGAGTTGGGGCTCTACCAAGTGTGGCAACTGAGAACGGTTTCAACCTGTGATCTCTACTGGTGG
 ACAGCCAGGACCAGACCCCTGGCCTGGATCCTGAACGGCAGTCAGTCCCTGGGAGCAGTGTGAAGGTCCGTTGA
 CCAGGGTCAGTGGTGGGCCCTGGCTGCCAGCAGTCTACTGGCCCATTTGTCACTGTCACTGCTCT
 TTGCTTACTGTGCTTCAAGGAGCCCTCATCATCCTCGTGGCTCCCTTGAGAGCAGTCCGGCTCGGGCAAGG
 TTCAGGGCTGTGAGACCCCTGCCAGTGTGGACGCTGACAACAAGTGCCTAGGCAGTGAGGTAGCT**TAA**ACTCTAGGCA
 CAGGCCGGGGCTGGGTGCAGGCACCTGGCCATGCTGGCTGGGCCAACGGCCACTGGGACTAGGATGACAG
 CAGCACAAAAGACCACCTTCTCCCTGAGAGGAGCTTGTACTGTCATGATGACACTCAGCAGGGTG
 ATGCACAGCAGTCTGCCTCCCTACACTGATATTGAAGAACCTGGAGAGGATCCTCAGTCTGGCATTCCAGGGACCC
 CCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTCAGTCTGGCATTCCAGGGACCC
 CAGAAACACAGTGTTCAGAGAACCTAAAAACCTGCCAGGAAACTCCACTCTGAAGCTGCCCTTGGAACACCAACACT
 TAAACAAATCATATGCTAACATGCCACTCTGGAAACTCCACTCTGAAGCTGCCCTTGGAACACCAACACT
 TCTCCAGGGTCATGCAGGGATCTGCTCCCTCTGCTTCCCTTACCAAGTCGTGCACCGCTGACTCCCAGGAAGTC
 TTTCCCTGAAGTCTGACCACCTTCTTGCTTACCAAGTCGTGCCCTGGCAGACTCTGATCCCTCTGCCCTGGCAGAATGG
 CAGGGTAATCTGAGCCTCTTACCTTACCCCTAGCTGACCCCTCACCTCTCCCCCTCCCTTTCCTTGT
 TTTGGGATTCAAGAAAATGCTGTGAGAGACTGTTATTAAATATAAGGCTTAAAAAA

FIGURE 158

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQQLQLLLPTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ
DFDTLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGMTNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFF
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGCSVGPSSDKALTFMHDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLV
YLGTTGSLHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTOGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPEPESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA

```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTAGCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGGCTTCGTAGAAG
 TGAGC**ATG**GCTGGGCAGCGAGTGCTCTTAGTGGCTTCTCCCTGGGTCTGCTC
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGGTTCTCAGATTCTCAAGATCACGGTCATAATGTCACCATGCTAACCAAAAGAG
 GTCCTTTATGCCAGATTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAAGAGAATTAAAAAGAGTTGATTCTTCTGGAAGAAACTTTAGG
 TGGCAGAGGAAAATTGAAAACTTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
 ATTTTTAAATAGAAAGGATATCATGGATTCTAAAGAATGAGAACTTCGACATGGTGATA
 GTTGAACATTGACTACTGTCCTTCTGATTGCTGAGAAGCTGGGAAGCCATTGTGGC
 CATTCTTCACTTCATTGGCTCTTGGATTGGCTACCAATCCCCTGTCTTATGTT
 CAGTATTCCGTTCTGACTGATCACATGGACTCTGGGGCCGAGTGAAGAATTTCCTG
 ATGTTCTTAGTTCTGAGGAGCAACAGCACATGCAGTCTACATTGACAACACCATCAA
 GGAACATTACAGAAGGCTAGGCAGTTGCTCATCTTCACTGAAAGCAGAGTTG
 GGTCATTAACCTGACTTGCCTTGATTGCTCGACCTCTGCTCCCAACACTGTTAT
 GTTGGAGGCTTGATGGAAAACCTATTAAACAGTACCACAAGACTTGGAGAACTTCATTG
 CAAGTTGGGACTCTGGTTGTCCTGTGACCTTGGCTCCATGGTGAACACCTGTCAGA
 ATCCGAAATCTCAAGGAGATGAACAAATGCCCTTGCTCACCTACCCAAGGGGTGATATGG
 AAGTGTCACTGTTCTCATTGCCAAAGATGTCACCTGGCTGCAAATGTGAAATTGTGGA
 CTGGCTTCTCAGAGTGACCTCCTGGCTACCCAAGCATCCGTCTGTTGTCACCCACGGCG
 GCCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGATCCCTCT
 GGAGACCAGCCTGAAAACATGGTCCAGTAGAAGCCAAAAGTTGGTGTCTATTGAGT
 AAAGAAGCTCAAGGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGGCAGTGGCTGCCAGTGTCTCGCCTCCACCGCTCAGCCCCACACAG
 CGGCTGGTGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCAGCACCTCAAGCCCTA
 TGTCTTCAGCAGCCCTGGCATGAGCAGTACCTGTCACGTTTGTGTTCTGCTGGGGC
 TCACTCTGGGACTCTATGGCTTGTGGAGCTGCTGGCATGGCTGTCTGGTGGCTGCGT
 GGGGCCAGAAAGGTGAAGGAGACA**TAA**GGCCAGGTGCAGCCTTGGGGGTCTGTTGGTGG
 GCGATGTCACCATTCTAGGGAGCTTCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTC
 TAGTTATCTCTGTTCTGAAGAACAGGAAAATGCCAAAATCATCCTTCCACTTGC
 TAATTTGCTACAAATTCTACCTTACTAGCTCTGCCTGCTAGCAGAAATCTTCCAGTCCT
 CTTGTCCTCTTGTGCTGCATCAGCAAGGGCTATGCTGTGATTCTGCTCTGAGTGACTTG
 GACCACTGACCCCTCAGATTCAGCCTTAAACCCATGTCACGCTCTCCGAA
 TCACACCCCTGACTCTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCACTCCGCCCC
 TACTATCTATCATGAAATAACATCCAAGAAAGACACCTGTCATATTCTTCAGTTCTGTT
 TGTTCTCCACATATTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAAGGGC
 CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTGGTGCCACAGTGAGCTCCT
 TCTGGCTGAGCAGGCATGGAGACTGTAGGTTCCAGATTCTGAAAATAAAAGTTACA
 GCGTTATCTCCCCAACCTCACTAA

FIGURE 160

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLLGVFLLPGVLLSEAAKILTISTVGGSYLLMDRVSQILQDHGNVTMLNHKRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIDMSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIPLSYVPV
FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKAELWF
INSDFAFDFARPLLPTVYVGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVIWKCQCSHWPKDVKLAANVKIVDWLPQSDLLAHPSTIRLFVTHGGQ
NSIMEAIQHGVPVMVGIPLFGDQOPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDVFVFLGLT
LGTLWLCGKLLGMAVWWLRGARKVKET
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTGGGGATTTGAAGAGAGGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTCTGTCACACCCGTACACACACATACCATGTT
 CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGCCATCCAGCAGGGCTACCCCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCAGGCTTCATCCCTCCTTCTCTCCAAAGCCCA
 ACTGCTGTCAGTGCATGCTGCCAAGGAGGGAACTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGACACAGGTATGGAGAGGGGTTAGCGAGCCTAGAGAGGGC
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGA
 AGACCGGGCACTTGTGGGTGCAGAGCCCCTCAGCC**ATG**TGGGAGCCAAGCCACACTGGC
 TACCAGGTCCCTACACAGTCCCGGGCTGCCCTGGTTCTGGTGCCTCTGCCCTGGGGC
 GGGTGGGCCAGGAGGGTCAGAGCCGTCTGCTGGAGGGGAGTGCCTGGTGTCTGTGA
 GCCTGGCCAGCTGCTGCAGGGGCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGC
 GAGTGGCATTGCTGCGGTCCGAAGCACCACATGAGCCAGCAGGGAAACCGGCAATGGC
 ACCAGTGGGCCATCTACTCGACCAGGTCTGGTGAACGAGGGCGGTGGCTTGACCGGGC
 CTCTGGCTCCTCGTAGCCCTGTCCGGGGTGTCTACAGCTCCGGTTCCATGTGGTGAAGG
 TGTACAACCGCAAACGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTATCTCAGCC
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACAGCTGTGCTACTGCCCTTGG
 CCCTGGGGACCGAGTGTCTCGCCTCGCTGGGGAAACTACTGGTGGTTGGAAATACT
 CAAGTTCTCTGGCTTCATCTTCCCTCT**TGA**GGACCAAGTCTTCAAGCACAAGAAT
 CCAGCCCCCTGACAACCTTCTGCCCCCTCTGCCCCAGAAACAGCAGAGGAGAGAG
 ACTCCCTCTGGCTCCTATCCACCTCTTGCATGGACCCCTGTGCCAAACACCCAGTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTCCACCCACCCACCCAGTTAC
 CTCCCAGCCACCTGCTGCATCTGTTCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTGGCA
 AGAAGGAAGATCTGCACTACTTGCAGGCTCTGCTCTCCGGTCCCCACCCAGCTTCC
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCCAG
 ATGGACAAGCCTCAGCGTACCTGCAGGCTTCTCCTGTGAGGAAAGCCAGCATCACGGATC
 TCAGCCAGCACCGTCAGAACGCTGAGCCAGCACCGTATGGGCTAGGGTGGAGGCTAGCCAC
 AGGCAGAAGGGTGGGAAGGGCTGGAGTCTGGCTGGTGGAGGAAGGAGGGTGTATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGCTCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAAAACATCGATAACCAGTCATCCTTGTGCTGGCCACCTCCTGAAACTGCTCCAC
 CTTGAAAGTTGAACCTTCTGCTCCACACTCTGACTGCTGCCTCCTCCTCCAGCTCTC
 TCACTGAGTTATCTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTGAT
 CTGTGCTGCTTATCTCCTCTTAGGCTTCTATTACCTGGGATTCCATGATTCAATTCTT
 CAGACCCTCTGCTGCCAGTATGCTAAACCTCCCTCTCTTCTTCTTATCCGCTGCCCATT
 GGCCCAGCCTGGATGAATCTATCAATAAAACAACAGAGAATGGTGGTCAGTGAGACACTAT
 AGAATTACTAAGGAGAAGATGCCTCTGGAGTTGGATCGGGTGTACAGGTACAAGTAGGTA
 TGTTGCAGAGGAAAATAATCAAACGTATACTAAATTAAAAA

FIGURE 162

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVILLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFAANDPDVTREAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
```

Signal peptide:

amino acids 1-32

FIGURE 163

GCTGTTCTCGGCCACCACTGGCCGCCGGCGCAGCTCCAGGTGTCCTAGCCGCCAGC
 CTCGACGCCGTCCCCGGGACCCCTGTGCTCTGCGCGAAGCCCTGGCCCCGGGGCCGGGCAT
 GGGCCAGGGCGCGGGTGAAGCGGCTTCCCAGGGCGTGAAGGGCTTCAGCC**AT**
GAAAGACCCTCATAGCCGCCTACTCCGGGTCTCGCGCGAGCGTCAGGCCAGGCTGACC
 GGAGCCAGCGCTCTCACGGAGGACCTGCGCTGCGCGAGGGCTGGGAGATGGGCACT
 GGATCCAGCAGCATCCTCTCCGCCCTCCAGGACCTTCTGTCACCTGGCTCAATAGGTCAA
 GGTGGAAAAGCAGCTACAGGTACAGGTACATCTCAGTGCTCCAGTGGTCCTGCTTGTACTGG
 GAGTGGCCTGCAGTGCCATCCTCATGTACATATTCTGCACTGATTGCTGGCTCATCGCTGTG
 CTCTACTTCACTGGCTGGTGTGACTGGAACACACCCAAGAAAGGTGGCAGGAGGTACA
 GTGGGTCCGAAACTGGCTGTGTGGCGCTACTTCGAGACTACTTCCCATCCAGCTGGTGA
 AGACACACAACCTGCTGACCACCAGGAACCTATATCTTGGATACCACCCCCATGGTATCATG
 GGCCTGGGTGCCTCTGCAACTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTCCCAGG
 CATA CGGCCTTACCTGGCTACACTGGCAGGCAACTCCGAATGCCGTGTTGAGGGAGTACC
 TGATGTCTGGAGGTATCTGCCCTGTCA GCCGGACACCATA GACTATTGCTTCAAAGAAT
 GGGAGTGGCAATGCTATCATCATCGTGGTCGGGGTGGCGCTGAGTCTTGAGCTCCATGCC
 TGGCAAGAATGCAGTCACCCCTGCGGAACCGCAAGGGCTTGTGAAACTGCCCTGGCTCATG
 GAGCTGACCTGGTCCCCTACTCCTTGGAGAGAATGAAGTGTACAAGCAGGTGATCTC
 GAGGAGGGCTCTGGGCCATGGTCCAGAAGAAGTCCAGAAATACATTGGTTGCC
 ATGCATCTCCATGGTCGAGGCCTCTCTCCGACACCTGGGGCTGGTGCCTACTCCA
 AGCCCATCACCACGTGGAGAGGCCATCACCACCCAGCTGGAGGCCCTGGTGAAGCTTCGACAAGCA
 CAAGACATCGACCTGTACCAACCATGTACATGGAGGCCCTGGTGAAGCTTCGACAAGCA
 CAAGACCAAGTCGGCTCCGGAGACTGAGGTCTGGAGGTGAAC**TGA**GCCAGCCTCGGG
 GCCAATTCCCTGGAGGAACCAAGCTGCAAATCACTTTTGCTGTAAATTGGAAGTGTCA
 TGGGTGTCTGTGGTTATTTAAAAGAAATTATAACAATTGCTAAACAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAA

FIGURE 164

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNR
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIAVLYFTWLVDWNTPKGGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMGGICPVSRDTIDYLLSKNGSGNAIIVVGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPYSGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPTIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN
```

Important features of the protein:

Transmembrane domain:

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 165

GGGCGGGCGGGATGGGGGCCGGGGCGGGCGCCGCACTCGCTGAGGCCCGACGCAGGGCCGGCCGGCC
 GGGCGAGGAGCGCAGCGGGCCAGAGCGGGCCGCGAGGCAGGCCGGGACGCCGCGACGAGCAGGTGGCG
 GCGCTGCAGGCTTGTCCAGCCGAAGCCCTGAGGGCAGCTGTTCCACTGGCTCTGCTGACCTTGTGCCTTGA
 CGGCTGCCTCAGCAGGGCCGTGCACCCGCTCTGAGCAGCGCC**ATG**GGCCTGCTGGCCTTCCTGAAGACCCA
 GTTCGTGCTGCACCTGCTGGTCGGCTTGTCTCGTGGTAGTGGCTGGTCATCAACTTGTCCAGCTGTGCAC
 GCTGGCGCTGGCCGGTCAGCAAGCAGCTCACCGCCCTCAACTGCCGCTCGCCTACTCACTGGAGCCA
 ACTGGTCATGCTGCTGGAGTGGCTGCACGGAGTGTACACTGTTCACGGACCAGGCCACGGTAGAGCGCTT
 TGGGAAGGAGCACGCAGTCATCATCCTCAACCACAACCTCGAGATCGACTTCCTGTGGGTGGACCATGTGA
 GCGCTCGGAGTGTGGAGCTCCAAGGTCTCGTAAGAAGGAGTGTCTACGTGCCCTCATGGCTGGAC
 GTGGTACTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGAGGAGGACCGGGACACCGTGGTGAAGGGCTGAG
 GCGCCTGCGACTACCCGAGTACATGTGGTTCTCCTGACTGCGAGGGACCGCCTCACGGAGACCAAGCA
 CCGCGTTAGCATGGAGGTGGCGCTGCTAAGGGCTTCCTGCTCAAGTACCACTGCTGCCGCGAACAGGG
 CTTCACCAACCGCAGTCAGTGCCCTCGGGGACAGTCGAGCTGTATGATGTAACCTGAACCTCAGAGGAAA
 CAAGAACCCGTCCTGCTGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTAGGGAGATTCCTCT
 GGAAGACATCCCCTGGATGAAAAGGAAGCAGCTCAGTGGCTCATAAACTGTACCAGGAGAAGGACCGCCTCCA
 GGAGATATAATCAGAAGGGCATGTTCCAGGGGAGCAGTTAACGCTGCCGGAGGCCGTGGACCCCTCTGAA
 CTTCTGTCTGGCCACCATTCTCTGTCTCCCTCTCAGTTGTCTGGCGTCTTGCCAGGGATCACC
 TCTCTGATCCTGACTTCTGGGTTGTGGAGCAGCTCAGTGGCTTGGAGTTCGAGACTGATAGGAGAATCGCT
 TGAAACCTGGGAGGTGGAGATTGCA**G**CAGTGGACTGAGATGGCATCACTGTAACAGCCTAGGCAACAGAGCAAGACT
 CAGTCTAAAAAAAAAAAAACAAAAACCCCCAGAAATTCTGGAGTTGAACCTGTAGTTACTGACATGAAAA
 ATTCACTAGAGGCTGAACAGCAGATTGAGCAGGAGAAAAATCAGCAAGCTGAAGATGGTACCTTGAGATT
 TTTCAGGCTAATGAAAAAGAATGAAGGAAATTAAACAGCCTCAGAGACCCATGGCACCCTCACACAAATCAA
 CATATGCATGATGAGAGTCCCAGAAGGAGAGGAGAGAAAGGGTCAGAAAGAATGCCACAAGCTGATGAAAAACA
 GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTCAT
 AATCAAAGTGTCAAATGACAAGAATCTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTCAAAGGATCTTG
 ATCAGATTAACAGCTCATTTCTCCTCAGAAATCATGGGAGCCAGGGAGATGTGGGATGAACACTGTTGAAGGAA
 AACCTCAACTGTAATTATTGGACTTTGAGTCTTAGATGGCCTGACCTCTTGTCTCAGGGACAGTTTCA
 ATTTAATCCCTAATAACAATTAGTCAGCTCAGGCTGACCTGTAGGAAGGCCGTCTTAGGCCGGCACAGTGGC
 TTACACCTGTAATCCCAGCACTTGGGAGGCCAGACGGGTGGATCATTTGGGTCAGGCTGATCTCAAACCTCCT
 GAGTCAGGTGATCTGCCGCCTCAGCCTCCAAAGTGTGATTGAGCAGGCGTGAGCCACTGCGCTGCCGG
 ATTTCTTTAAGGCTGAATGATGGGGCCAGGCACGATGGCTACGCCGTGATCCAAGTAGCTGGATTGTA
 AACATGCACCACCATGCCCTGGCTAATTTGTATTTTAGAGAGACGTGTTAGCCAGGCTGGCTCGATCTCCT
 GACCTCAAGTGACCACCTGCCCTCAGCCTCCAAAGTACTGGGATTACAGGCGTGAGCCACTGCGCTGCCCT
 GCATCTGTGATGTGCTTATTGCCATTGTATATCTCTATCTTGGGAAATGTCTGTTCAAGTCCTTGC
 CCTTTAAATTTATTATTATTATTGAGACAGGGCTTGTGTTCTGGCCAGGCTGGAGTA
 CAGTGGCACAGTCTGGCTCACTGCAGCCTGCCAGCTGGCTGAGTGTACCTCCCACCTCAGCCTCCCT
 AGCTGTATTTGTATTTGTAGCTGAGCTGAGTTGTATTTGTGGAGACAGCATTCAACCAG
 TGCCCAGGCTGGCTTGAACCTCTGAGCTCAAGTGTACCTGCTGCCCTCAGCCTCCAAAGTGCTGGGATTACAGA
 CATGAGCCACTGCACCTGGCAAACCTCCAAATCAACACACACACACACACACAC
 GAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTGGCATGAGAAGTCGAGGCTG
 CAGTGAAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCCTGTCT

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVVSGLVINFVQLCTLALWPVSKOLYRRLNCRLAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFIEDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLYHLLPRTKGFTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGVRRLIGESLEPGRWRLQ
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTATTTAAGAACCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCCTGGGGCA
 GCCACCAGGCATATTCATCTTGTGTGTTTCTTTGCTTAGCAGTGGGGCACTTCTT
 GCTTATTTCTTGGTAGGAAAGGGGCTCAGTTGTCTTGTGGGGTGGCAGGCAGGCCG
 GCTTACGCCTGATAACGGCCCTGGGTTAGAAGGGAAAGGAAAGATAAAACTTTATAACAAATGGG
 GATAGCTGGGTCTGAGACCTGCTTCAGTAAAATTCTGGATCTGCCTATAACCTTCTT
 TTCTCTAACCTGGCATACCCCTGCTTAAAGCCTCTCAGGGCTCTCTGTCTTAGGATCAA
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCTGGCAGCTTCATTGT
 ACATGTGGTGTCTCTGTCTTG**TAA**TGTGGTATGCCATGGGTCTTGCACAAGCCT
 TTCCTCTTGGCTGGACACTGTTCCCTGCCCTGCCCTGGCAGCTTCATTAAATGTAGTC
 ATCCTGCAGATTCAATTCTAACATCATTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
 CTTGTTTAATGCTCTCATAAGACCCTTGTTCCCTTGCAGCACTGCCACTCAGTTGTA
 TCTTATGTGCGTTGTGGTTGTATGGGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC
 TGCCTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT
 CATGTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCAGTCACCA
 GATGGTGTAGGGCCAGCATTGTAATTACACGTTGACTGTGCTGTGAATTATCTGGGA
 TGCAGGTCTGATTCACTGGCCAGGTGGCATCTCTAACAAACTCCCACGTGATGCTGA
 TGCTGGCCTATGAACTATACTAAATAGTAAGAACATCTATGGAGCCAGGCTGGCATGGTGGC
 TCACACCTATGATCCCAGCAGCTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCCAACATGGTGGAACCCATCTGTACTAAAAATACACAAATTAGCTG
 GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAACCGCTT
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAAAAAAAAAAA

FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRHIHLCVCFSFALALGHFLLISLVGKGLSLSGVGGRQAGLRLIRPWVRR
EGKINFYTNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPEWSWS
GPCPPGQLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACTCCTGGTCCCAGTGATCCACCGCCTCAGCCTCCAAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGCCCTCTGAACAACTTTTCAAGCAACTAAAAAGCCAC
 AGGAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTAGTGCTCCTACTCCTACCTAC
 ATTAAAATCTGTTTTGTTCTCTGTAACTAGCCTTACCTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGCCAACCTGACCTCACTCTGGAACGAGAACAGAGGTTCTACCCAC
 ACCGTCCTCGAAGCCGGGACAGCCTCACCTGCTGCCCTCGCTGGAGCAGTGCCTC
 ACCAACTGTCTCACGTCTGGAGGCAGTGACTCGGGCAGTCAGGTAGCTGAGCCTTGGTA
 GCTGCGGCTTCAAGGTGGCCTGCCCTGCCGTAGAAGGGAT**TGA**CAAGCCCAGAAGATT
 CATAGGCGATGGCTCCACTGCCAGGCATCAGCCTGCTGTAGTCATCACTGCCCTGGGG
 CCAGGACGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCGCCAT
 CTAACCTTTCATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACCTGTCCCAAGG
 AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCATTCTCCTGGAACATGAGGGAACGCCGGAGGAAGCAAAGTGGCA
 GGGAAAGGAACATTGTGCCAAATTATGGGTCAAGAAAAGATGGAGGTGTTGGTTATCACAAGGC
 ATCGAGTCTCCTGCATTCACTGGACATGTGGGGAAAGGGCTGCCGATGGCGATGACACACT
 CGGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCCGATCCACGTACAGCTGCTG
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAATCTGCGATCACCAG
 CCAGGGCAGCCGTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCTCCTCCCTC
 TGAGAGGCCCTCTATGTCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGCTAATG
 GCTCAGTGTGGCCAGGAGGTCAAGCAAGGCCTGAGAGCTGATCAGAAGGGCTGCTGTGCG
 AACACGGAAATGCCTCCAGTAAGCACAGGCTGAAAATCCCCAGGAAAGGACTGTGTGGCT
 CAATTAAATCATGTTCTAGTAATTGGAGCTGCCCCAAGACCAAAGGAGCTAGAGCTTGGT
 TCAAATGATCTCCAAGGGCCCTATAACCCAGGAGACTTGATTGAATTGAAACCCCCAAA
 TCCAAACCTAAGAACCAAGGTGCATTAAGAATCAGTTATGCCGGGTGTTGGCCTGTAATG
 CCAACATTTGGGAGGCCGAGGCAGGCTAGATCACCTGAGGTCAAGGAGTTCAAGACCAGCCTG
 GCCAACATGGTGAACCCCTGCTCTACTAAAAATACAAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
 GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAATAAAAAAGAATTATGGTTATTGTAA

FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRD
```

Signal peptide:

amino acids 1-15

FIGURE 171

GCGGGCCCGAGTCCGAGACCTGTCCCAGGAGCTCACGTGACCTGTCAGTGCCTC
CCGCCGCCTCCTGCCCGGCCATGACCCAGCCGGTCCCCGGCTCTCCGTGCCCGCCGCT
GGCCCTGGGCTCAGCCGCACTGGCGCCGCCCTGCCACTGGCCTCTCCTGGGGAGGCGGT
GCCCCCCATGGCGAGGCCGGCGAGAGCAGTGCTGCTGCTTCCCCCGAGGAACAGCCGCCTGTGG
CAGTATCTTCTGAGCCGCTCCATGCAGGGAGCACCCGGCGTGCAGCAGCTGCTGAC
CCTGGAGCAGCCGCAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTTGGCCAACC
TGGCGCGGCTCATCCAGGCCAAGAACGGCGCTGGACCTGGCACCTCACGGGCTACTCCGCC
CTGGCCCTGGCCCTGGCGCTGCCCGGGACGGCGCGTGGTACCTGCGAGGTGGACGCGCA
GCCCCCCGGAGCTGGACGGCCCTGTGGAGGCAGGCCGAGGCCGAGCACAAAGATGACCTCC
GGCTGAAGCCGCCTGGAGACCCCTGGACGAGCTGCTGGCGGGCGAGGCCGGCACCTTC
GACGTGGCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
GCTGCTGCGACCCGGAGGCATCCTGCCGTCTCAGAGTCCTGTGGCGGGAAAGGTGCTGC
AACCTCCGAAAGGGGACGTGGCGGCCAGTGTGCGAACCTAAACGAACGCATCCGGCGG
GACGTCAAGGGTCTACATCAGCCTCCTGCCCTGGCGATGGACTCACCTGGCCTCAAGAT
CTAGGGCTGGCCCTAGTGAGTGGCTCGAGGGAGGGTTGCCTGGAACCCCCAGGAATTGAC
CCTGAGTTAAATTGAAAAGTGGGCTGGGACACAAAAAAA

FIGURE 172

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAAALALGAAAFATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSLRLLTLLEQPQGDSSMMTCEQAQLLANLARLIQAKKALDLGFTGYSALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRLKPALETLDELLAAGEAGTFDVAVVDA
DKENCSAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

CCGCCGCCGCAGCCGCTACCGCCGCTGCAGCCGCTTCGCCGGCCTGGGCCTCTGCCGTCA
 GCATGCCCACACGCCCTCAAGCCCAGGGACTTGGTGTGCTAAGATGAAGGGCTACCCTCAC
 TGGCCTGCCAGGATCGACGACATCGCGATGGGCCGTGAAGCCCCCACCAACAAGTACCC
 CATCTTTCTTGGCACACACGAAACAGCCTCCTGGGACCCAAGGACCTGTTCCCTACG
 ACAAATGTAAAGACAAGTACCGGAAGCCAACAAGAGGAAAGGCTCAATGAAGGGCTGTGG
 GAGATCCAGAACAAACCCCCACGCCAGCTACAGGCCCTCCGCCAGTGAGCTCCTCCGACAG
 CGAGGCCCGAGGCCAACCCGCCAGGCAGTGACGCTGACGAGGACGATGAGGACCGGG
 GGGTCATGCCGTACAGCGTAACGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA
 GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCCTGCCTAAAGATGTC
 GGTCTCGAAACGAGCCGAAAGGCCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG
 AAGAGGAGAACTCGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCAGGACTTCACACCT
 GAGAAGAAAGCAGCGGTCCGGGCCACGGAGGGCCCTCTGGGGGACGGAAAAAAAAGAA
 GGCGCCGTAGCCTCCGACTCCGACTCCAAGGCCATTGGACGGGCCAACGCTGAGCCGG
 TGGCCATGGCGCGGTGGCGTCCTCCCTCCCTCTCCCTCCCTCCGACTCCGATGTG
 TCTGTGAAGAAGCCTCCGAGGGCAGGAAGCCAGCGGAGAAGCCTCTCCGAAGCCCGAGG
 GCGGAAACCGAACGCTGAACGCCCTCCGTCCAGCTCAGCAGTGACAGTGACAGCGACGAGG
 TGGACCGCATCAGTGAGTGGAAAGCGGGGAGGCGCGAGGGCGAGCTGGAGGGCCGG
 CGCGCGAGAGCAGGAGGAGGAGCTGCGCGCCTGCCGGAGCAGGAGAAGGAGGAGAAGGA
 GCGGAGGCCGAGCGGGCGACCGCGGGAGGCTGAGCGGGCAGCGCGCAGCAGCGGGG
 ACGAGCTCAGGAGGACGATGAGCCGTCAAGAACGCGGAGCAGCAAGGCCGGGGGG
 CCCCCGTCTCTCTGACTCCGAGCCGAGGCCAGCTGGAGAGAGAGGCCAACGAAATCAGC
 GAAGAACGCCAGTCTCAAGCACAGAGCCGCCAGGAAACCTGCCAGAACGGAGAACGAG
 TGCGGCCCGAGGAGAACACAAGCCAAGCCGTGAAGGTGGAGCGGACCCGAAGCGTCC
 GAGGGCTCTCGATGGACAGGAAGGTAGAGAACGAAAGAGCCCTCCGTGGAGGAGAACG
 GCAGAACGCTGCACAGTGAGATCAAGTTGCCCTAAAGGTCGACAGCCGGACGTGAAGAGGT
 GCCTGAATGCCCTAGAGGAGCTGGAACCCCTGCAGGTGACCTCTCAGATCCTCCAGAAC
 ACAGACGTGGTGGCCACCTTGAAGAACGATTGCCGTTACAAAGCGAACAAAGGACGTAATGGA
 GAAGGCAGCAGAACGAGTCTATAACCGGCTCAAGTCGCGGGCCTCGGCCAACAGATCGAGGCGG
 TGCAGAAAGTGAACAAGGCTGGATGGAGAACGGAGAACGGCGAGGAGAACGCTGCCGGGAG
 GAGCTGGCCGGGGAGGAGGCCAGGAGAACGGCGGAGGACAAGCCAGCACCAGCTCTC
 AGCCCCAGTGAATGGCGAGGCCACATCACAGAACGGGAGAGCGCAGAGGACAAGGAGCACG
 AGGAGGGCTGGGACTCGGAGGAGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGACAGC
 GTACGGGAGGGTCCCGACCTGGACAGGCCTGGAGCGACGGCAGGAGCGCAGAGGGCAGC
 GGGGGACTCGGAGGCCCTGGACGAGGAGAGCTGAGCCGCCGGCAGCCAGGCCAGCCCCGC
 CCGAGCTCAGGCTGCCCTCTCCCTCCGGCTCGCAGGAGAGCAGAGCAGAGAACGAGA
 GAACGCTGTGCTGTTGTATTGTTCCCTGGTTTTTCTGCCTAATTCTGTGATT
 TCCAACCAACATGAAATGACTATAACGGTTTTAATGA

FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNNKYPPIFFFGTHTAFLGPKDLFPYD
KCKDKYGKPNKRKGFGNEGLWEIQNNPHASYSAPPVSSSDSEAPEANPADGSDADEDDERG
VMAVTAVTATAASDRMESDSDKSSDNGLRKTPALKMSVSKRARKASSLDQASVSPSE
EENSESSSESEKTSQDFTPEKKAAVRAPRRGPLGGRKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDVSVKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSDSDSDEV
DRISEWKRRDEARRRELEARRREQEEELRRLREQEKEEKERRERADRGEAERGGGGSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKSAKKPQSSSTE PARKPGQKEKRV
RPEEKQQAKPVKVERTRKRSEGFSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMEEAAEVYTRLKSRLGPKIEAV
QKVNKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGEESAEDKEHE
EGRDSEEGPRCGSSELDHDSVREGPDLRPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTTCTCCTGGATCTCACCTAACCAACTGCAGATCTGGGACTCATCAGCCTCAATAATTATATTAAATTA
 ACACCATTGAAAGAGAACATTGTTCAT**TAG**AATGCTAATAAAGATGAAAGACTTAAAGCCAGAACCCAAGA
 TTTCACCTTTCTGCTTGATGATGCTAACCATGACCATGTTCTTCAGTCAGTCAGTCAGTCAGTCAGTCATC
 AAATATTCCAAGACTCAAGCTAACCATCAAAGACTGCTGCTTCAAATAGCTGTATTCCCTTTGGGTTCATC
 AGAAGGACTGGATTTCAAACTCTCTCTTAGATGAGGAAAGAGGCTGCTTGGGAGCCAAAGACCACAT
 CTTCTACTCAGCTGGTGACTIONAAACAAATTAAAGAAGATTATTGGCCTGCTGCAAAGGAACGGGTGGA
 ATTATGTAATTAGCTGGGAAAGATGCCAATACAGAACATGCTAAATTGAGTCTGGCAGACTGAAATGCTTGGAGTCAAGGAA
 AACTCACATATATGTTGAGTCTGGAGCATTCATCCAATATGTTGAGTCTGGCAGACTGAAATGCTTGGAGTCAAGGAA
 GGATATTATATTCAAACAGACACATAATTGGAGTCTGGCAGACTGAAATGCTTGGAGTCAAGGAA
 TTTGCTTCAGTAATGACAGATGAGTACCTCTACTCATGACCAACACTACAGAACATGACATTTCAGAGCACTACTGGCTCAATGG
 AGCAAAATTATTGGAACCTTCTCATACCAAGACACACTACAATCCAGATGATGATAAAATATATTCTTCTTCTG
 TGAATCATCTAAGAAGGCAGTACCTCCGATAAAACCATCCTTCTCGAGTTGGAAGAGTTGTAAGAATGATGT
 AGGAGGACAACGCAGCCTGATAAAACAAGTGGACACTTTCTTAAGGCCAGACTGATTGCTCAATTCTGGAAG
 TGATGGGGCAGATACTTACTTTGATGAGCTCAAGATATTATTACTCCCCACAAGAGATGAAAGAAATCCTGT
 AGTATATGGAGTCTTACTACAACCAGCTCCATCTCAAAGGCTGCTGTTGTGTATAGCATGGCTGACAT
 CAGAGCAGTTTAATGGCCATATGCTCATAGGAAAGTGCAGACCATGTTGGGTGAGTATGATGGGAGAAT
 TCCTTATCCACGGCCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCGAGATTTCAGA
 TGATGTATCAGTTCTAAAGCAGCAGTCTGTGATGATAAGTCCGTATACCCAGTTGCAAGGAGGACCAACGTT
 CAAGAGAATCAATGTGATTACAGACTGACACAGATAGTGGTGGATCATGTCATTGCAAGAAGATGGCAGTACGA
 TGTATGTTCTGGAACAGACATTGGAACCTGCTCAAAGTGTGAGCATTCAAAGGAAAGTGGAAATATGGA
 AGAGGTAGTGTGGAGGAGTTGCAAGACTCATCAATCATTTGAAACATGGAATTGCTCTGAAGCA
 GCAACAATTGTACATTGGTCCCAGAGATGGATTAGTTGCACTCTCCTGACAGATGCGACACTTATGGGAAAGC
 TTGCGCAGACTGTTGCTGCCAGAGACCCACTGTGCTGGGATGGAAATGCTCTCGATATGCTCCTAC
 TTCTAAAAGGAGAGCTAGACGCAAGATGTAATGCGACCCATCACCAGTGCTGGGACATCGAAGACAG
 CATTAGTCATGAAACTGTCATGAAAGGTTGCAATTAACTCAACCTTCTGAAATGTTACCC
 TAAATCCAACAGCAACTATTAAATGGTATATCCAGAGGTCAGGGGATGAGCATGAGAGGAGTTGAAAGCCGA
 TGAAAGAATCATCAAAACGGAATATGGCTACTGATTGCAAGTTGCAAGAAGAAGGATTCTGGGATGTTACTG
 CAAAGCCCAGGAGCACACTTCATCCACACCATGTAAGCTGACTTGAATGTCATTGAGAATGAAACAGATGGA
 AAATACCCAGAGGGCAGAGCATGAGGAGGGGAGGTCAAGGATCTATTGGCTGAGTCACGGGAGGAGATCAAAGA
 CTACATCCAATCCTAGCAGCCCCAAACTTCAGCCTCGACAGACTGCGAACAGATGTGGCACAGGGAGAAGCG
 GAGACAGAGAAACAAGGGGGCCAAAGTGGAAAGCACATGCAAGGAAATGAAGAAGAAACGAAATCGAAGACATCA
 CAGAGACCTGGATGAGCTCCCTAGAGCTGAGCCACG**TAG**TTTCTACTTAATTAAAGAAAAGAATTCTTAC
 TATAAAAACATTGCTCTGTTGTATATCCCTATAGTAATTCTAAATGCTTCCATGGAGTTTGCTAAGG
 CACAAGACAATACTGAATAAGACAATATGTGATGAAATATAAGAAAGGGCAAAAATTCTTGAACCAGTTT
 CCAAGAACAAATCTGCACAAGCAAAGTATAAGAATTATCCTAAAAATAGGGGTTACAGTTGAAATGTTTA
 TGTGTTGAGTTTGGAAATTATTGTCATGTAATAGTTGAGCTAAGCAAGCCCCGAATTGATAGTGATAAGGT
 GCTTTATCCCTCGAATGTCATGAAATTACCATGCACTGTTGTGCTATGTTCTTATGAAACAGATATA
 CATCCATTGAGAACCCAGCTACCTTGTGAGGAAATAAGAGGTCAAGCACAAATTAAAGACAACCTCCATTATC
 AACAGGAACCTCTCAGTGAGGCCATTCACTCTGGAGAATGGTATAGGAATTGGAGAGGTGCAATTCTTCT
 TGGCCACTGGGTTAAATTAGTGTACTACACATTGATTACTGTTAGAGGGCAACTATGTTCCCCCAGGATTCT
 ATTGACTAGTCAGGAGTAACAGGTTCACAGAGAGAAGTTGGCTTAGTTATGTTTTAGAGTATATACTAA
 GCTCTACAGGGACAGAACATGCTTAATAAATCTTAATAAGATATGGAAAATTCTTAAATAAAACAAGGAAAACA
 TAATGATGTATAATGCTCCTGATGGGAAGGCATGCAAGATGGGATTGTTAGAAGACAGAGGAAAGACAGCCAT
 AAAATTCTGGCTTGGGAAAACATCATATCCCCATGAAAGGAAGAACATCACAAATAAGTGAAGAGTAATGAA
 TGGAGCTCTTCACTAGGGTATAAGTAGCTGCCAATTGTAATTCTGTTAAAAAAATCTAGATTATAACCA
 AACTGCTAGCAAAATCTGAGGAAACATAAATTCTCTGAAAGAACATAGGAAGAGTAGACATTTTATTATAACC
 AATGATATTCTAGTATATTTCTCTCTTTAAAAAAATTCTACTCTGTATATTGAGTGAATAGGAGAAAACAATATAACACAGA
 GAATTAAGAAAATGACATTCTGGGAGTGGGATATATTTGTTGAATAACAGAACAGAGTGTAAAATTAAAC
 AACGGAAAGGGTTAAATTAAACTCTTGACATCTCACTCAACCTTCTCATTGCTGAGTTAATCTGTTGAATT
 GTAGTATTGTTTGTAAATTAAACAATAAAGCCTGCTACATGT

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLQNIPLRKLTYKDLLLNSCIPFL
GSSEGLDFQTLLLDEERGRLLLGAKDHFIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGFHPICGYIDLGVYKEDIIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPYDHHYIRTIDISEHYWLNGAKFIGTF
IPDTYNPDDDKIYFFFRESSQEGSTSDFKTLISRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSIKEKWNMEEVLE
LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYCAWDGNA
CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHEADEKVIFGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYYCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRNRRHDLDELPRAVAT
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGGGTCATCCTGGAGCATGCCAACCGCGGGGAGCAGA
 CAACCTCCCAGGTAAAGCTGGGAGCAAGACCTGAAGCTGTTCTCAGGAGCCTGGTGTATTTCACCCAC
 CTCAGCAGTTCAGCCAGCAGGGACTGATCAGGTGTGTCCTGGAGTGGGAGCAGAAGCGTGGCTGGCAAGA
 GTGGCCTGGAGAAAGAGGTTCAGCGCTTGACCAGCGAGCTGCCGTGACTACAAGATCCAGAACCATGGGCATC
 GGGTAGGGGGGGCACAGGTGTATGTGACCTTCTGTCAAGCAAGAAGAGCTGAGAGAGGGATCTTGG
 AGCCATTGAGGGTGTATGGAGCTACAGAGGGAGGGAAAGGTATTTAAGTAACAGTGTGGCACAAATAGTTAA
 GAGCACAGTTTGGAGCTAGACCGACATAGGTCATAATTCTCTGTGCTCCTAGTCTGTAGCCCCAGGT
 AAGGGAGTGAACCTAACCTCTGGACTTCATTTCCATCACTAAAGTAGGGCAATAATAGCACCCACCTCAT
 AGGAAGATTAATGACATAATGTATGTG**ATG**CAACTAGCAAAGTACCAAGTCCATAGTAAGTCATGCCACAG
 TATTTCACCCACCCCTTCTCTGCCTCCACCAGGTACTGCAACGACTGGAGCAGAGGGCGCAGCAGGCTT
 CAGAGCGGGAGGCTCAAGCATAGAACAGAGGTTACAGGAAGTGCGAGAGAGCATCCGCCGGCACAGGTGAGCC
 AGGTGAAGGGGCTGCCCGCTGGCCCTGTCAGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
 TGACCCAGGCCAGGATGAGGTGGAGCAGGAGCGGGCTCAGTGAGGCTCGGTGTCAGGAGCTGGCTGCC
 CAACCGCTGAGGATGCTGAGCTTCTGACTTGAGGAATGTGAGGAGACGGAGAGCTTTGAGGAGCCTGCC
 CCCAACCCCTGGCACGAGGCCCTCCCTGCCCTGCACACGTGGTATTCGCTATCAGGCAGGGCGTGGAGATG
 AGCTGACAATCACGGAGGGTAGTGGCTGGAGGTATAGAGGAGGGAGATGCTGACGAATGGTCAAGGCTCGGA
 ACCAGCACGGCAGGGTAGGCTTGTCCCTGAGCGATATCTCAACTTCCCGACCTCTCCCTCCCAGAGAGCAGCC
 AAGACAGTGACAATCCCTGCGGGCAGAGCCCACAGCATTCTGCACTACAGCTACACCCGGACAGA
 GTGCAGAGGAGCTGAGCTTCCCTGAGGGGCACTCATCCGCTGTCGCCCCGGCCAAGATGGAGTAGATGAC
 GCTTCTGGAGGGGAGAATTGGGGCGTGTGGGTCTCCCTCCCTGCTGTTGGAAGAGCTGCTGGCCCC
 CAGGGCACCTGAACCTGACCCCTGAACAGATGCTGCCGCCCCCTCTCCCTCCAGCTCTCCCACTGCA
 CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCCTGCTGGGACAAGCCCTGGACTCTCCCTGGGTTCTGG
 ACATGATGGCACCTCGACTCAGGGCATGCGTCCACCCCTGGCTAAAGGCCGGATCTGGGCC
 CAGATCCCCCACCT**TGA**AGGCCAGGGAAAGCCTGACCCCCAGTGTGCTGTCCTATCTCAAGCTGTCAGA
 CCACACCATCAATGATCCAGAGCAACAGCAAAAGCTGGAATGCCCTTATTCCACCCCTCACCTCAAGGGT
 GGAAACTTGCCCCCTCCCATTTCTAGAGCTGGAACCCACTCCTTTTCCATTGTTCTATCATCTTAGGACC
 GGAACACTACCTTCTCTCTGTATGACCCCTATCTAGGGTGGTGAATGCTGAAATCTGGGCTGGAAAC
 ATCCATCAAGGTCTAGTAGTTCTGGCCACCTCTTCCACCCCTGGCTCATGACCCACCCACTCTGGATG
 CCAGGGTCACTGGGTTGGGCTGGGAGAGGAACAGGCCCTGGGAATCAGGAGCTGGAGCAGGATGCGAAGCAG
 CTGTAATGGCTGAGGGATTATTGACAATGAATAAAGGGCACGAGGCCAGGGCAGGGCTGGGCTCTGTG
 CTAAGAGGGCAGGGGCTACGGTGTATTGCTTAGGGGCCACACGGGAGGGCTGCTCCAGTGGC
 GCTCTATCATATGGAGCGAGGTGTGGGAAGGGGGAGGGCAGGCAGCCTGTTGCAAGGAGGGAAAGAGAC
 TGAGGGGCTGTGACCTCTGAGGCCCTGAGACTGTGCAACTCCAGGTGGAAAGTAGAGCTGGTCCCTC
 AGCTGGGGGAGGTGCTGTCAGTGGAGGGCTTCACGCCACCCACCCCTGGCCTGCCAGCTGGTAG
 TCCATCAGCACATGAAGGAGACTTGGAGAAGAGGAAGATAACACTGTTGCTCCTGTTCAAGCTGTG
 TTTCCCTGGGCTCAGGACCTCCCTACCTCACCAACCAAGGGATTATAGCAAAGGCTAACGCTGC
 AGTTTACTCTGGGGTTCAGGGAGCCAAAGGCTTAAATAGTTAAGTAGGTGATGGGAAGATGAGATTACCTCA
 TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGAACACCTGAGAGAACAGGG
 TCAACAATGAGAGACCCAGGAGTAGGTCTACCTGATCAGAGTGTCTGGTTGCTGGCTGCCATTGCTTGA
 AGTCCCGGCTGTGTTCTACCTGGTATCAGAGTGTCTGGCTGGCTGCCATTGCTTGAAGTGG
 GCAGGCCCTGGGCTTGGGCCCCCTCCCGGCCCTCAGTGGCTGCTGGCTGCCCTCCCCAGACCCCTG
 TCTCAGGGGGCAGGCCCTCCCATGGCAGGCATCCCTGCCCTGGCTGCCCTGGGAGCCATCAGGTG
 CAGGGGGTCTGGCTGCCATTCTGTACTGGGGCTGGCTAGGACCTGGGCTGTGGCAGTC
 TCTCAATGTGTGTCACCCGGAACCTGGAGGGAGGGAAACACTGGGTTAGGACCAACTCAGAGGCTG
 GCCCTCCCTCTGACCCAGGACATCTGAGTTGGCTACTTCCCTCTGGCCTAAGGTAGGGAGGC
 AGATTGTGGGGCACATTGTGATGCTGACTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCC
 TTGGGATCAGGTGCCTGATCACTGGCCCCCTACCTCAGCCCCCTTCCCTGGAGC
 ACCTGCCCAACTGCCCA
 CAGAGAACACAGTGGTCTCCCTGTCGGGGGGCGCTTTCTCTGGAGCGTCCCTGACGGACAAGTGGAG
 GCCTCTGCTCGGGCTGCAATGGATGCAAGGGCTGCAAGAGCCAGGTGCACTGTG
 GATGATGGGAGGGGCTC
 CGTCCTGCAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGAGTGA
 GGGTAACATTCCATT
 TCATGTTTGTCTTACGTTCTCAGCATGCTCTTAAACCCAGAACGCCCAATT
 TTTCTGTCTTATCTAATAACTCAATATTAAG

FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFRYQAGREDELTITEGEWLEVIEEGDAEW
VKARNQHGEVGFVPERYLNFPDLSLPESSQDSNPGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRGVFPSSLVEELLGPPGPPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPAAKADPGHPDPLT
```

FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGGAGAAAGAGACAGAGACAAAGGCACAGCGGA
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCAGACAGAGTCCTACAGAGGGAGAGGCCAGAGAAGCTGCAGA
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAGGGCTCAGGAGGAGAGTTGGAGAACGCCAGACCCCTGG
GCACCTCTCCAAGCCCAGGACTAAGTTCTCATTCTTAACGGTCCTCAGCCCTCTGAAAACATTG
TCTGACCTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGCTTCCAAGCTAGGGTGTGGAGGACTTGGT
GCCCTAGACGGCCTCAGTCCCTCCAGCTGCAGTACAGTGC~~ATGT~~CCAGACAGGCTCGCATCCCAGGGAGGGG
CTTGGCAGGGCGTGGCTGTGGGAGGCCAACCTGCCTCTGCTCCCTATTGTGCCCTCTGGCTGGTGTG
GCTGCTCTGCTACTGCTGGCCTCTCCTGCCCTCAGCCGGCTGGCAGCCCCCTCCCCGGAGGAGGAGAT
CGTGTTCAGAGAAGCTCAACGGCAGCGTCCTGCCCTGGCTCGGGGCCCTGCCAGGCTGTTGTGCCGCTTGCA
GGCCTTGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCAGGGCTGACAGTGCAGTA
CCTGGCCAGGCGCTGAGCTGCTGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC
GGAGTCGGTGGCATCTCTGCACTGGATGGGGAGCCCTGTTAGCGTGTACAATATCGGGGGCTGAACCTCCA
CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACACTGCTGGGGACCTGGGCTCACATCCTACGCCGGAAGAGTCC
TGCCAGCGGTCAAGGTCCCAGTGTCAACGTCAAGGCTCCTTGGAAAGCCCCAGGCCAGACCCCGAAGAGCCAA
GCGCTTGCTTCACTGAGTAGATTGTGGAGACACTGGTGGTGCAGATGACAAGATGGCGCATTCCACGGTGC
GGGGCTAAAGCGTACCTGCTAACAGTGTGGCAGCAGCAGCCAAGGCCCTAACAGCACCCAAAGCATCCGAATCC
TGTCAAGCTTGGTGGTACTCGGCTAGTGTGATCCTGGGCTCAGGCAGGGAGGGGCCCAAGTGGGGCCCAAGTGGTGC
CCAGACCCCTGCGCAGCTCTGTGCCCTGGCAGCGGGGCCCTAACACCCCTGAGGACTCGGGCCCTGACCATTG
CACAGCCTTCTGTGTTACCCGTCAGGACCTGTGTTGGAGGATGATGGGCTCAGCTCAGGCTTCACTGCTGCTCA
CACCGCTGTCGACCCGGCTGGAGCTGTGCCATTGTGGAGGATGATGGGCTCAGCTCAGGCTTCACTGCTGCTCA
TGAACCTGGGTCATGCTTCAACATGCTCATGACAACCTAACAGCATGCACTGAGTTGAATGGGCTTGGACAC
CTCTCGGCACTGTCATGGCCCTGTGATGGCTCATGGTGGATCCTGAGGAGCCCTGGTCCCCCTGCACTGCCGCT
CATCACTGACTTCTGGACAATGGCTATGGGCACTGTCTCTAGACAAACAGAGGCTCCATTGCACTGCCGCT
GACTTTCCCTGGCAAGGACTATGATGCTGACGCCAGTGCAGCTGACCTTGGGCCACTCACGCCATTG
ACAGCTGCCGCCCTGTGCTGCCCTCTGGTGCCTGGCCACCTCAATGCCATGCCATGTGCCAGACCAAACA
CTCGCCCTGGGCCATGGCACACCCCTGCGGCCAGCAGGCCATGGGCTGCATGGTGGTGCCTCCACATGGACCA
GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGCTTGGGACCATGGGCTGACTGCTCTGGACCTG
TGGGGTGGTGTCCAGTTCTCCTCCGAGACTGCACGAGGCCCTGTCAGGCGATGCCATCTGGGCTGACCTTCCGCAG
CCGCCGTACCGCTTCCGCTCTGCAACACTGAGGACTGCCAACACTGGCTCAGCCCTGACCTTCCGCAGGAGCA
GTGTGCTGCCATAACACCACCGCACCTCTCAAGAGCTTCCAGGGCCATGGACTGGGTCTCGCTACAC
AGGCGTGGCCCCCAGGACCACTGCAAACACTCACCTGCCAGGCCGGCAGTGGCTACTACTATGTGCTGGAGCC
ACGGGTGGTAGATGGGACCCCTGTCCTCCGGACAGCTCCTCGGTCTGTGTCAGGGCGATGCCATCCATGCTGG
CTGTGATCGCATATTGGCTCCAAGAAGTGTACAAGTGCATGGTGTGCGGAGGGAGCGGTTCTGGTGTG
CAAGCAGTCAGGCTCCTCAGGAATTAGGTACGGATAACAAATGTGGTCACTATCCCCGGGGGCCACCCA
CATTCCTGTCGGCAGCAGGAAACCCCTGGCACCCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA
TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCTGGGCACTGAGCTTGC
CACGCCGACTGCAGCCTCAGAGACACTGTCAGGCCATGGCCACTGCCAGCCTTGACACTGCAAGTCT
AGTGGCTGGCAACCCCAAGGACACGCCCTCGATACAGCTTCTCGTGCCTGGGCCAGCCCTCAACGCCACG
CCCCACTCCCCAGGACTGGCTGCCAGGAAAGAGCACAGATTCTGGAGATCCTCGGCCGGCGCCCTGGCGGGCAG
GAAA~~TAA~~CCCTCACTATCCCGCTGCCCTTCTGGCACCGGGCTCGGACTTAGCTGGAGAAAGAGAGAGCTT
CTGTTGCTGCCCTAGCTAACAGACTCAGTGGGAGGGCTGTGGCGTGAAGACTGCCCTCTCTGCCCTAAT
GCCGAGGCTGGCCCTGCCCTGGTCTGGGAGGGCACTGATGGGTTAGTGGATGGAAGGGGCTGACAGAC
AGGCCCTCATCTAAACTGCCCTCTGCCCTGCCAGGAGGGGAAGGCAGGGAGGGCTGGGCC
CAGTTGATTATTAGTATTACTTCTTCTTCTTCTGGGAGGGCACTGATGGGTTAGTGGATGGAAGGGGCTGACAGAC
CCTGACCCCTGACCCCTCATGCCCTGCCAGGGCTGGGAGGAATCCAGGGTGGTGTGATAGGTATAAGTGGT
TGTGTATGCGTGTGTGTGTGAAAATGTGTGTGCTTATGTATGAGGTACAAACCTGTCTGCTTCTC
TTCCCTGAATTATTATTGGAAAAGAAAAGTCAGGGTAGGGTGGGCCCTCAGGGAGTGAGGGATTATCTTT
TTTTTTTTCTTCTTCTTCTTCTTCTTCTTCTGGAGACAGAATCTCGCTCTGCGCCAGGCTGGAGTGC
GCACAATCTCGGCTCACTGCATCCTCCGCCCTCCGGGTTCAAGTGATTCTCATGCCCTCAGGCCCTGAGTAGCT
GGATTACAGGCTCCTGCCACGCCAGCTAACATTGGTGTGTTGGAGACAGAGTCTCGCTATTG
ACCAGGGCTGGAATGATTCACTGCACCTCGCCACCTGGGTTCCAGCAATTCTCCTGCCTCAGGCC
CGAGTAGCTGAGATTAGGCACCTACCAACGCCGGCTAACCTGGGAGGGCAAGGACTAGGGTCTGGGAA
CATGTTGGCCAGGCTGGTCTGAACCTGACCTTAGGTGATCCACTGCCCTCATCTCCAAAGTGC
ACAGGCGTGGACCGCACCGTGCTGGCACGCCAACTAATTGGTGTATTAGTAGAGACAGGGTT
TGGCCAGGCTGCTCTGAACTCCTGACCTCAGGTAATCGACCTGCCCTGCCCTCCAAAGTGC
TGTGAGGCCACCGCCGGTACATATTAAATTGAAATTCTACTATTATGTGATCCTTGGAGTCAGACAG

FIGURE 179B

ATGTGGTTGCATCCTAACTCCATGTCCTGAGCATTAGATTCTCATTTGCCAATAATAATACCTCCCTAGAAG
TTTGTGAGGATTAATAATGTAATAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAGGAAA
AAAAAAAAAAAAAAAAGGAAA

FIGURE 180

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLASLLPSARLASPLPREEEIV
FPEKLNGSVLPGSAGAPARLLCRLQAFGETLLEQDSGVQVEGLTVQYLGQAPELLGGAEP
GTYLTGTINGDPESVASLHWDGGALLGVLQYRGAEHLHQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPMCNVKAPLGSPSPRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAKAKFKHPSIRNPVSLVVTRLVLIGSCEEGPVQGPSAAQTLRSFCAWQRGLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
NSKPCISLNGPLSTSRRHMAPVMAHVDPPEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PTVPGKDYDADRCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFNI PQAGGWGPWGPGDCSRTCGGGVQFSSRDCTRVPVRNGGKY
CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMWDVPRYTGVAPQDQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNVVTIPAGATHILVRQQGNPGHSIYLALKLPDGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTPQDWLHRRAQILEILRRRPWAGRK
```

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
 CAAAGAACCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTAAATCC
 AAGAAAATATGTAAATCACTTAAGATTGTGGACTGGTGTGGTATCCTGGCCCTAACTCT
 AATTGTCCCTGTTGGGGAGCAAGCACCTCTGCCGGAGGTACCCAAAAAGCCTATGACA
 TGGAGCACACTTCTACAGCAATGGAGAGAAGAAGAGATTACATGGAAATTGATCCTGTG
 ACCAGAACTGAAATATTCAAGCGAAATGGCACTGATGAAACATTGAAAGTGCACGACTT
 TAAAAACGGATAACACTGGCATCTACTTCGTGGTCTTCAAAAATGTTTATCAAAACTCAGA
 TTAAAGTGATTCTGAATTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
 ACAACTTTCTTGAAACAGTCAGTGATTGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
 TTTCTTAAAATTCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATC
 CCACTCTAAATATCAGTTCTGAGTTACAAGACTTGGAGGGAGGAGAAGATCTTCACTTT
 CCTGCCAACGAAAAAAAAGGGATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAAGT
 AGAGAAGACCGTCAGCCAGACAAGCAAGTGAGGAAGAACTCCAATAATGACTATACTG
 AAAATGGAATAGAATTGATCCCAGCTGGATGAGAGAGGTTATTGTTGATTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCGCGTGTGAACCTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACGAGTCATCTGCGTGTACATGCCCTGTAAGGGTGGTGGCCCC
 GCATGCTGGGGAGGGTCT**TAA**TAGGAGGTTTGAGCTCAAATGCTAAACTGCTGGCAACATAT
 AATAATGCATGCTATTCAATGAATTCTGCCTATGAGGCATCTGGCCCCCTGGTAGCCAGCT
 CTCCAGAATTACTGTAGGTAAATTCTCTCTTCATGTTCTAATAACTTCTACATTATCACC
 AAAAAAAAAAAAAAAA

FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEETTTFFEQSVIWVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEEEDLHPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEEELPINDY
TENGIEFDPMLERGYCCIYCRRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCAGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGCACC**ATG**GCCAGCACGGCGTGCAGCTCTGGGCTTCCT
 GCTCAGCTTCCTGGCATGGTGGCACGTTGATCACCAACATCCTCACGGCGTGTCTACCTGAAAGGGCTCTGGATGGAG
 CAGCGCACGTGGCACCAACATCCTCACGGCGTGTCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCGCCCTCATGGTCATCTCCTGCCTGCTCTGGGCATAGCCT
 GCGCCTGCCGTATCGGGATGAAGTGCACCGCCTGCCAAGGGCACACCCGCCAAGACC
 ACCTTGCCATCCTCGCGGCACCCCTTTCATCCTGGCCGGCTCCTGTGCATGGTGGCGT
 CTCCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGCCCTCGCTATTGGT
 GGCACCCCTGCTTGCCTGTCCTGCCAGGACGAGGCACCCCTACAGGCCCTACCAGGCCCGCC
 CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
 ACAATGGGCCCCCTCAGTGACCTGCCACGCACAGCGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCTGGCTGCTGTGGCTGGGTCCCCGGCGGGACTGTC
 AATGGAGGCAGGGTTCCAGCACAAAGTTACTTCTGGCAATTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTAGAGGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
 AGCTCTCTATACCAAAGACTGAAAAAAAATCCTGTCTGTTGTATTATTATATAT
 TTATGTGGGTGATTGATAACAAGTTAATATAAGTGAATTGGAGTTGGTCAGTGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGCAGGATGTGGCTGTTATGAAAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGLTITLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL
FILAGLLCMVAWSWTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLCLSCQ
DEAPYRPYQAPPRATTANTAPAYQPPAAYKDNRAPSVTSAHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCTCAGGAGCGCGTTAGCTCACACCTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCGCAGGGCGGCCAGGATC**ATGT**CCACCACATGCCAAGTGGTGGCGTTCCT
 CCTGTCCATCCTGGGGCTGGCGGCTGCATCGCGGCCACCAGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCATTTCACCATCCTGGACTTCCAGC
 CATGCTGCAGGCAGTGCAGGCCATTGATGATCGTAGGCATCGTCCTGGGTGCCATTGCCCTCC
 TGGTATCCATCTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGATCATGTTCATGTCTCAGGTCTTGTGCAATTGCTGGAGT
 GTCTGTGTTGCCAACATGCTGGTACTAACTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTTCAGACCAGGTACACATTGGTGCAGCTGTGTTCGT
 GGCTGGGTGCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATGCCCTGCCGGGG
 CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTCTATCATGCCCTCAGGCCACAGTGTG
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTGGTCCAACACCAAAAACAAGAAG
 ATATAACGATGGAGGTGCCGCACAGAGGACGAGGTACAATCTATCCTCCAAGCACGACTA
 TGTG**TAA**TGCTCTAACGACCTCTCAGCACGGCGGAAGAAACTCCGGAGAGCTCACCAAAA
 AACAAAGGAGATCCCCTAGATTCTTGCTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTCGATTTCATCTTGGAGAGGCCAAATGGCTTAGCCTCAGTCTGTCTAAATATTCC
 ACCATAAAACAGCTGAGTTATTATGAATTAGAGGCTATAGCTCACATTCAATCCTCTAT
 TTCTTTTTAAATATAACTTCTACTCTGATGAGAGAATGTGGTTTAATCTCTCTCAC
 ATTTGATGATTAGACAGACTCCCCCTTCCCTAGTCAATAAACCCATTGATGATCTA
 TTTCCAGCTTATCCCCAAGAAAATTGGAAAGGAAAGAGTAGACCCAAAGATGTTATT
 CTGCTGTTGAATTGCTCCCCACCCCAACTGGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTGTAATCTCCAGGCCATGATCTGGTTTCTACACTG
 TGATCTAAAAGTTACCAAACCAAAGTCATTTCAGTTGAGGCAACCAACCTTCTACTG
 CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCTCCACTGGAG
 TCCTCTTCTGCGGGTCAGAAATTGTCCTAGATGAATGAGAAAATTATTTTTAAT
 TTAAGTCCTAAATATAGTAAATAAATAATGTTTAGTAAATGATACACTATCTGTGA
 AATAGCCTACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTGACATTGTCT
 ATATGGTACTTGTAAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTGGAGGCTGAGGAGGAAGGATCACTTGAGGCCAGAAGTTCGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCATGGT
 GCATACACCTGTAGTCCCAGCATTGGAGGCTGAGGTGGAGGATCACTTGAGGCCAGGG
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAAATAAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA
 ACTAATTCTTAA

FIGURE 186

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pi: 8.50, NX(S/T): 1
MSTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFCASTGFGSNTKNKKIYDGGARTE
DEVQSYP SKHDYV
```

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAAACTGTTCTCTTGTGGCACAGAGAACCCCTGCTCAAAGCAGAAGTAGCAGTTCCG
 GAGTCCAGCTGGCTAAAACATCCCAGAGGATA**ATG**CAACCCATGCCTAGAAATCGCTG
 GGCTGTTCTGGTGGTGAATGGTGGGCACAGTGGCTGTCACTGTATGCCTCAGTGG
 AGAGTGTGCCCTTCATTGAAAACAACATCGTGGTTTGAAAACCTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG
 CTCTTCTCGGACCTACAGGCAGCCAGAGGACTGATGTGCTGCTCCGTATGTCCTTC
 TTGGCTTCATGATGCCATCCTGGCATGAAATGCACCAGGTGCACGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTCATCACGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
 GTGCCCAAAACGTGAGCTGGAGAAGCTCTACTTAGGATGGACCACGGCACTGGTGCT
 GATTGTTGGAGGAGCTCTGTTCTGCGTTTGTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACTTCCCACATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGTG**TAG**TTGTATGTTTTAACTTACTATAAAGC
 CATGCAAATGACAAAAATCTATATTACTTCTAAAATGGACCCAAAGAAACTTGATTAA
 CTGTTCTTAACTGCCTAATCTAATTACAGGAACTGTGCATCAGCTATTATGATTCTATAA
 GCTATTCAGCAGAATGAGATATTAAACCAATGCTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTCTAAGGTGGTTCAAGCATCTACTCTTTATCATTACTTCAAAATGACATTGCT
 AAAGACTGCATTATTTACTACTGTAATTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACATTATCTCACATAGAGACATGCTTATATGGTTATTTAAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTCAGGGAAATCATGGATAGGTTG
 AAGAAGGTTACTATTAATTGTTAAAACAGCTTAGGGATTAATGTCCTCCATTATAATGA
 AGATTAAAATGAAGGCTTAATCAGCATTGTAAGGAAATTGAATGGCTTCTGATATGCTG
 TTTTTAGCCTAGGAGTTAGAAATCTAACCTTCTTATCCTCTTCCCAGAGGCTTTTT
 TTCTTGTGTATTAAATTAACATTTAAAACGCAGATATTGTCAGGGCTTGCATTCA
 AACTGCTTTCCAGGGCTACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTGATG
 GTTTAGGAAAGTGAAAATATTTGTTTGATTGAAGAAGAATGATGCATTGACAA
 GAAATCATATATGTATGGATATATTAAATAAGTATTGAGTACAGACTTGAGGTTCATC
 AATATAAATAAAAGAGCAGAAAATATGCTTGGTTTCACTTGTACCAAAAAACAAACA
 ACAAAAAAAAGTTGTCCTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTC
 AAAATTGTCATTGTTCTGTGAAAATAAATTCCTCTTGTACCACTTCTGTTAGTTACTAAA
 ATCTGTAAATACTGTATTTCTGTTATTCAAATTGATGAAACTGACAATCCAATTG
 AAGTTGTGTCGACGTCTGCTAGCTAAATGAATGTGTTCTATTGCTTATACATTATA
 TTAATAAATTGTACATTTCTAATT

FIGURE 188

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSIFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCC**ATG**GCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGCTGGTG
 AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTCATCGGAAACAGCAT
 CGTGGTGGCCCAGGTGGTGTGGAGGGCCTGTGGATGTCTGCGTGGTGCAGAGCACCGGCC
 AGATGCAGTGAAGGTGTACGACTCACTGCTGGCGTGCACAGGACCTGCAGGCTGCACGT
 GCCCTCTGTGTCATGCCCTCCTGTGGCCCTGTTGGCTGCTGGTCTACCTGCTGGGC
 CAAGTGTACCACCTGTGGAGGAGAAGGATTCCAAGGCCGCCGGTGCACCTCTGGGA
 TTGTCTTGTCATTCAGGGGCCTGACGCTAACCGCTGGCTGAGGCCAAAAGCAGGAGCTGGGGCCTCCCT
 ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCATTACATGGCCCGCTACTCAACATCTGCCCT
 CTACTTGGGCTGGGGGGCCTCAGGCCTTTGTTGCTGGTGGGGTTGCTGTGCTGCACCT
 GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCT
 GCCATCTCTCGGGGGCCCTGAGTACCCCTACCAAGAATTACGTC**TGA**CGTGGAGGGAAATG
 GGGGCTCCGCTGGCGCTAGGCCATTCCAGAAGTGGCAGTGCCAACAGCTTGGATGGGTT
 CGTACCTTTGTTCTGCCTCCTGCTATTTCTTGACTGAGGATATTAAAATTCAATT
 GAAAAGTGGAGCCAAAGAGGGGATGCTTGAGATTCTGGATCTGACATGCCCATCTAGAAGC
 CAGTCAGCTATGAACTAATGCCGGAGGCTGCTTGCTGTGCTGGCTTGCAACAAGACAGAC
 TGTCCTCAAGAGTTCCCTGCTGCTGGCTGGGGCTGGCTCCCTAGATGTCAGTGGACAGCTG
 CCCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTTCACCCCTGGAAAAACAAATCATCTG
 TTAACAAAGGACTGCCACCTCCGAACTTCTGACCTCTGTTCCCTCGTCTGATAAGACG
 TCCACCCCCCAGGGCCAGGTCCCAGCTATGAGACCCCCGCCACCTCCAACACTGCACC
 CTTCTGCCCTGCCCTCGTCTCACCCCTTACACTCACATTATCAAATAAGCATG
 TTTTGTAGTGCA

FIGURE 190

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTS
FVISGVTLIPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGPSPHYMARYSTSAPAIISRGPSEYPTKNYV
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAAGGCTCCACGTTCTACATCTTG
AGCATCTTCTACCACCTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTATCCC
TTGCAAATTGCTGGGCTGGTCTTGGGCTTGGCATGGTGGGACTCTGCCACAACCCT
TCTGCCTCAGTGGTGGAGTATCAGCTTTGTTGGCAGCAACATTATTGTCTTGAGAGGCTC
TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
TAGCTCCTTGGCTCTCCCGCCTGCCCTGAAACAGCCCAGGCCCTCATGTGTGGCTG
TTGCTCTCTCCTTGATGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
GGCTCTAACGAGAGGGCAAAGCATACTTCTGGAACTTCAGGAGTCCTCTTCATCCTGAC
GGGTATCTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA
ACCCAGCCATCCACATAGGTAGAAACGAGAGCTGGGAGCAGCACTTTCTGGCTGGCA
AGCGCTGCTGTCCTTTCATTGGAGGGGCTGCTTGTGGATTTGCTGCTGCAACAGAAA
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
ATACGACAATGCTTAGTAAGACCTCCACCAAGTTATGTCTAATGCCTCCTTGGCTCCAAGT
ATGGACTATGGTCAATGTTTTATAAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA
GAACCTGCTTATGTCTAGATTACATTGATACGAAAGTTCAATTGTTACTGGTGGTAGG
AATGAAAATGACTTACTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
GACCCAATCGCTGCTCCAATTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG
TGTACAATGATGGACTTATTACTTTGACCATCATGTATTATCTGATAAGAATCTAAA
GTTGAAATTGATATTCTATAACAATAAACATATACCTATTCTA

FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRKKQGYRYPVPGYRPHTDKRRNTMLSKTSTSYV
```

Important features of the protein:

Transmembrane domains:

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTCCAGC**ATG**AAGATCACTGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAAGTGGACTGCAGCATTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCATCA
CATACCTACCACTTGTGGTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC
GAGAGCTTGGAAAAGTAATGGAAGAGTCAGTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTCAGTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAAGAGTAATCTTG
ACTGAATGGAGAAAGTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCGCAT
TTTTTTTTAACACGTCAATAAAAAATAATCTCCCAGA

FIGURE 194

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9232, pI: 7.94, NX(S/T): 0
MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC
```

Signal peptide:

amino acids 1-19

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTGCCCTCCTGCTCGCGCCC
CGCCGCCATGGCTGCCTCCCCCGCGGGCCTGCTGTCCCTGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGCCAGGTGGCATAAGTGGAAATAACTCAAGCTGATGCTCAA
AAACGAGAACGACCTGTTCCAACTAAGACTAAAGTGGCGTTGATGAGAATAAGCAAAGA
ATTCCCTGGCAGCCTGAAGGCCAGAACGGCAGCTGTGGGACCGGACTGGCCCGAGGTGC
AGCAGTGGTACCAGCAGTTCTCATGGCTTGATGAAGCGAAATTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCTACGGCTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT
TCTTCATGTATCTCTTAATGCCTTACACTACTTGGTTCTGATTGCTCTATTCAGCAGAT
CTTTCTACCTACTTGTGTGATCAAAAAGAAGAGTTAAAACACATGTAAATGCCTTT
TGATATTCATGGGAATGCCTCTCATTAAAAATAGAAATAAGCATTGTTAAAAAGA

FIGURE 196

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
><subunit 1 of 1, 148 aa, 1 stop
><MW: 17183, pI: 8.77, NX(S/T): 0
MAASPARPAVLALTGLALLLLCWGPGGISGNKLKMLQKREAPVPTKTAVDENAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNRDRNGHEYGDYYQRHYD
EDSAIGPRSPYGFRHGASVNYDDY
```

Signal peptide:

amino acids 1-30

FIGURE 197

CGGCTCGAGCCGCCCGAAGTGCCCCAGGGGCCGATGGAGCTGGGGAGCCGGCGCTC
 GGTAGCGCGGCGGGCAAGGCAGGCGCCATGACCCCTGATTGAAGGGTGGGTGATGAGGTGAC
 CGTCCTTTCTCGGTGCTTGCCTGCCTTCTGGTCTGCCCTGCCTGGTCTAACGCACA
 CCGCTGAGGGCGGGACCCACTGCCAGCCGTAGGGACCCAAACGCCATCCCAGCCCAGC
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGAGGCCAGGGCAGAGACCCAGCCT
 GAGACACAGAGGTCAAGCTGCACAGCCAGCAGGCCACGGGTTCACAGAACACCGCCAG
 CCCCAGACTCCCCGAGGAGCCCTCGTGTACGGCTGAAATTCTCAATGATTAGCAGAGCAG
 GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTGAAAAGGACCCAGTTCCGGCCG
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCAGCACACCCAGACCCCTGG
 GCAGCCTTCACCTCCCTCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
 CCAAATCCCCCTGCCGCCGGGTCCGAGCCGCCCTCCGGCTGGAAATCGCAGCCT
 GCTGCTGCCCTGCTGCTCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGC
 CCTTCTTCCCTGACCGCCACTCTGGCCTGGCCGGCTCACCCCTGCTCCTCAGTCTCCTG
 GCCTTGCCATGTACCGCCGTAGGCCTCCGCCGGCGCTGGCAGCGTCGCCGGCCCTCC
 GGACCTTGCTCCCCCGCCGCCGGCGGGAGCTGCTGCCCTGCCAGGCCGCCCTCCGGCCTG
 CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCCGCCAGAGGACTCCGGGACTGGCGGAGG
 CCCCGCCCTGCGACCGCCGGGCTGGGGCACCTCCGGGCTGCTGAACCTCAGCCCGCA
 CTGGGAGTGGCTCCTCGGGTCGGGCATCTGCTGTCGCTGCCCTGCCGGCAGAGCCG
 GGCGCCCCGGGGCCGTCTAGTGTCTGCCGGAGGACCCAGCCGCCCTCCAATCCCTGAC
 AGCTCCTGGCTGAGTTGGGACGCCAGGTCGGTGGAGGCTGGTAAGGGAGCGGGAG
 GGGCAGAGGAGTTCCCCGAAACCGTGCAGATTAAAGTAAGTGTGAAGTTAAAAAAAAA
 AAAAAAAA

FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSMRGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVIRLKFLNDSEQVARAWPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGSEPGPSGLEIGSLLLPLLLLLLWYCQIQYRPFFPLTATLGLAGFTLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCCTAACGAACCATCAGCCC
TCAGCTGCACCTCCTCCCTCCAAGGATGACAAAGGCCTACTCATCTATTGGTCAGCAGC
TTTCTTGCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCAGGTGCTGCAGCT
GGAGGACTTGGATGGGTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTGTGG
AAAGCAAGTTAACATATCAAAGATAATGAAAATGCGGATGGAAGCTTGACTATGGCCTC
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCAACCTTCTGCAGGCATCCACTGCGAAAAAGGA
TTGTGTCCGGAGCACGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTAGGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCTGAGATGAAACAGGGTGCAGGTGCACCGTGG
AGTCATTCCAAGACTCCTGTCCTCACTCAGGGATTCTTCATTCTTCTCCTACTGCCTCCA
CTTCATGTTATTTCTTCCCTCCCATTACAACAAACTGACCAGAGCCCCAGGAATAAA
TGGTTTCTTGGCTTCCTCCTACTCCCATCTGGACCCAGTCCCTGGTCCTGTCTGTTAT
TTGTAAACTGAGGACCACAATAAGAAATCTTATATTATCG

FIGURE 200

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSILSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSLENLCHVDCQDLLNPNLLAGIHCAKRIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR
```

Signal peptide:

amino acids 1-18

FIGURE 201

TCTGACCTGACTGGAAAGCGTCCAAAGAGGGACGGCTGTAGCCCTGCTTGACTGAGAACCA
CCAGCTCATCCCAGACACCTCATAGCAACCTATTATACAAAGGGGAAAGAAAACACCTGAG
CAGAATGGAATCATTATTTTCCCAAGGGAGAAAACCGGGTAAAGGGAGGGAAAGCAATT
AATTGAAAGTCCCTGTGAATGGCTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC
TTGGGGTGAACACTTGGGTCTGTGGTTCTGATTGTAAGTGGAAAGCAGGTCTGCACACGC
TGTGGCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAAACTTCCAGGTGGAACAAGCA
ACCCATGTTCTGCTGCAAGCTGAAGGAGCCTGGAGGGAGAAAAGCTAAGTGAACATGAC
CTGTTGCATTGGCAAGTTCTAGCAAC**ATG**CTCTTAAGGAAGCGATAACAGGCACAGACCAG
CAGACTCCAGTTCTCCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT
TGCACCCCTCCCCACCACACCCTGCACCAGACTGTCACAGCCCAAGGCCAGCAAGCACAGCC
GAAGCCAGGTACCGCCTGGACTTGGGAATCCCAGGATTGGTACTGGAAGCTGAGGATGA
GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCCCTTATCTCACTGCGGGAGGATCAGC
TGCTGGTGGCCGTGGCTTACCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGG
AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGG
GGCTGATGAGGACGGGGAGGTGCTGAAGAAGAGGAGTTGACCCGTTCAGCCTGGACCCAC
GTGGCCTCCAGGAGGCACTCAGTGCCGATCCCCCTCCAGGGCTCTGCCGAGGTGCGG
CACCCACTGTGTCAGCAGCACCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG
TTTCCATGATGAGGCCTGGTCCACTCTCTGCGGACTGTACACAGCATCCTGACACAGTGC
CCAGGGCCTCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTAAG
TCTGCTCTCAGGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG
GCTGGGTGCCATCAGGGCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT
TCATGGATGCCACTCGCAGTGGCACCCAGGCTGGCTGGAGCCCTCAGCAGAATAGCT
GGTGACAGGAGCCAGTGGTATCTCCGGTATAGATGTGATTGACTGGAAGACTTCCAGTA
TTACCCCTCAAAGGACCTGCAGCGTGGGTGTTGACTGGAAGCTGGATTTCACGGGAAC
CTTGCCAGAGCATGTGAGGAAGGCCCTCAGTCCCCATAAGCCCCATCAGGAGCCCTGTG
GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTCCAAAACACTGGAGCGTATGACTC
TCTTATGTCGCTGCGAGGTGGTGAAAACCTCGAACTGTCTTCAAGGCCTGGCTGTGGTG
GCTCTGTTGAAATCCTTCCCTGCTCTGGTAGGACACATCTACCAAAATCAGGATTCCAT
TCCCCCTCGACCAGGAGGCCACCTGAGGAACAGGGTTCGATTGCTGAGACCTGGCTGG
GTCATTCAAAGAAACCTCTACAGCATAGCCAGGGCTCTCCTGAGCAAGGCTGAGA
AGCCAGACTGCATGGAACGCTTGAGCTGCAAAGGAGACTGGGTGCGACATTCACTGG
TTTCTGGCTAATGTCACCCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTCTCTGGAAA
GCTCCACAACACTGGACTTGGCTCTGTGCAGACTGCCAGGGCAGAAGGGGACATCCTGGGCT
GTCCCATGGTGGCTCTGCACTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC
AGGAAGGAGATTCACTTGGCAGCCACAGCACCTGTGCTTGCTGTAGGCAGGAGCAGG
GATTCTCAGAACTGCACGGAGGAAGGCCAGTGGCCATCCACCCAGCAGCACTGGGACTTCCAGG
AGAATGGGATGATTGTCACATTCTTCTGGAAATGCATGGAAGCTGTGGTGAAGAAA
AATAAAGATTGTACCTGCGTCCGTGTGATGGAAAAGCCGCCAGCAGTGGCGATTGACCA
GATAAAATGCTGTGGATGAACGA**TGA**ATGTCATGTCAGAAGGAAAAGAGAATTGGCCATC
AAAATCCAGCTCCAAGTGAACGTAAGAGCTTATATATTGATGAAAGCTGATCCTTTGTGT
GTGTGCTCTTGTGTTAGGAGAGAAAAAGCTCATGAAAGAATATAGGAAGTTCTCCTT
TCACACCTTATTGACTGCTGGCTGCTTA

FIGURE 202

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pi: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLLMLGCVLMVMVALHPPHHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKEAPKRDWGADEDGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTILLRTVHSILDTPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTFOYYPSKDLQRGVLDWKLDFHWEPLPEHVRKALQSPISPPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIYQNQDSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRRRLGCRTFWFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQQVILQNCTEEGLAIHQHQHWDFQENGMIHVILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFQINAVDER
```

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGAC**ATGGA**
 GTCCAGGATGTGGCCTGCGCTGCTGCTCCCACCTCCTCCCTCTGGCCACTGCTGTTGC
 TGCCCCCTCCCACCAGCCTGCTCAGGGCTTTCATCCTCCCTCGAACCCCCACCAGCCCCAGCC
 CGCCCCCCCCTGTGCCAGGGGAGGCCCTCGGCCCCACGTATGTGCGGTGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTGCCAAGTCTGCCTGGCACTG
 CACCCCCAGCCACCCATCAGGCTTGAGGAGGGGCCCTCATCCCAATACCCCTGGCT
 ATCGTGTGGGTCCACCGTGTCTCGAGAGGATGGAGGGACCCAACTCTGCCAATCCCAG
 ATTCTGGACTATGGTTTGAGGCCCTCATGGGCTCGAACCCCCACACCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGCTTATCCTGGAGAGGCACCTGCCACCCCTGCCATT
 CTGTTGGGGCCGTGGGAAGGTGTGGACCCCCAGCTCTATGTCACAATTACCATCTCCAT
 CATCATTGTTCTCGTGGCCACTGGCATCATCTCAAGTTCTGCTGGGACCGCAGCCAGAAC
 GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGACTCACCTACCCCCACCC
 TGACCATGAGGAGCCCCGAGGGGACCCCGGCCCTGGGATGCCCAACCCAAAGGGGCTCCAG
 CCTTCCAGTTGAACCGG**TGA**AGGGCAGGGCAATGGGATGGGAGGGCAAAGAGGGAAAGGCAAC
 TTAGGTCTTCAGAGCTGGGTGGGGTGCCTCTGGATGGGTAGTGGAGGAGGCAGGCAGTGGC
 CTCCCACAGCCCTGGCCCTCCCAAGGGGCTGGACAGCTCCTCTGGGAGGCACCCCTTC
 CTTCTCCAGTCTCAGGATCTGTGCTATTCTCTGCTGCCATAACTCCAACCTGCC
 TCTTTGGTTTTCTCATGCCACCTGTCTAAAGACAACCTGCCCTTTAACCTGATTCCC
 CCTCTTGTCTTGAACCTCCCTCTATTCTGCCCTACCCCTGGTTCTGACTGTGCCCTT
 TCCCTCTCCTCTCAGGATCCCCCTGGTAATCTGTGATGCCCAATGTTGGGTGCAGCC
 AAGCAGGAGGCCAAGGGGCCGGCACAGCCCCCATCCACTGAGGGTGGGCAGCTGTGGGA
 GCTGGGCCACAGGGCTCTGGCTCTGCCCTTGACACCACCCGGAACACTCCCCAGCC
 CCACGGCAATCCTATCTGCTGCCCTCTGCAGGTGGGGCTCACATATCTGTGACTTCG
 GGTCCCTGTCCCCACCCCTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTTCAC
 AGGCCATTGCACACGCTCTGCACCCCTCTCCCCGTCCATACCGCTCCAGCTGACTCT
 CATGTTCTCGTCTCACATTGCACTCTCTTCCACATTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTCTGCACACTTACCTCTCATGTGCTTCCGGCTGATGTTGGTGG
 TGTGCGGGCGTGCCTACTCTCCCTCATGAACACCCACCCACCTCGTTCCGCAGCCCTGC
 GTGCTGCCAGAGGTGGGTGGAGGTGAGCTGGGGCTCCTTGGGCCCTCATCGGTATGG
 TCTCGTCCCATTCCACACCATTGTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA
 TCACCCCTGAGGGCTCCCCCTGGGAATGGGGTAGTGTGAGGCCAGACTCACCCCCAGGCCA
 CTGCTAAATCTGTTCTGACAGATGGGTTTGGGAGTCGCCTGCTGCACTACATGAGAA
 AGGGACTCCCATTGCCCTCCCTTCTCACAGTCCCTTGTCTGTCTGCTGCCCTGGCTG
 TCTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCCCTCCAGCCT
 CCCTTGGGCCCTCCCTAACCTCCACCTAGGCTGCCAGGGACGGAGTCAGCTGGTTCAAGGCC
 ATCAGGGAGCTGCTCCACAGTCTACCCCTCCCTCCGGACTCCCTCTGCTCCCTGGCTCAGGTT
 CCTCCCTCCCTCACTGGTTTCCACCTCTCCCTCCCTTCTCCCTGGCTCCTAGGCT
 GTGATATATATTTGTATTATCTCTTCTTGTGGTGTGATCATCTGAATTACTGTG
 GGATGTAAGTTCAAAATTCAAATAAGCCTTGCAAGATAA

FIGURE 204

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTAAACCAGCGCAGTCCTCCGTGCGTCCC GCCGCGCTGCCCTCACTCCC GGCCAGGATGG
CATCCTGCTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCC GTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGAGCCCGTGGACACCGGTCCCC
CAGCCCCCACC GTCGCGCCAGGACCCGAGGA CAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGCGCTCGTGGTCGT CGC GCTGAGAAAGTTTCTGCCTCCTGAAGCGAATAAA
GGGGCCGCGCCGGCCGCGCGACTCGGCAAAAAAAAAAAAAA

FIGURE 206

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVAPGPEDSTAQERLDQGGGSLPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCGTTGGTGGTGC CGCGGCTGAAGGGTGTGGCGCAGCAGCGTCGGTGGTGGCCGGCG
 CGGGCCGGGACGGGCAATGGCCCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCA
 CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAAGTTCTCCTCTACCGCCACCATGTGA
 ACTTCAAGTCCTGGTGGGTGGCGACATCCCCGTGTCAGGGCGCTGCTCACCGACTGGAGC
 GACGACACGATGAAGGAGCTGCACCTGGCATCCCCGCCAAGATCACCCGGAGAACAGCTGGA
 CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGAAAGATGTACTTCC
 CCGGGTATTCCCCAACGAGCTGCGAAACATCTCCGGGAGCAGGTGCACCTCATCCAGAAC
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGAGGAGGGCAGCTCTCCAGGGAGGG
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATACCCCCGGGGACCTCCCCTAAGTAGCCC
 CCAGAGGCCCTGGGAGTGTGCCACCGCCCTCCCTGAAGTTGCTCCATCTCACGCTGGGG
 GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCAT
 CGACTGTCAGCACCGCTGTGGCATCTCCAGTACGAGACCATCTCTGCAACAACACTGCACAG
 ACTCGCACGTCGCCTGCTTGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
 GCCAGGGCCCTACTGTCCCTGGGTCCCAGGCTCTCCTGGAGGGGCTCCCCGCCTCCAC
 CTGGCTGTCATCGGGTAGGGCGGGGCCGTGGTTCAAGGGCGCACCACCTCCAAGCCTGTGT
 CCCACAGGTCTCGGCCAGTGGAAAGTCAGCTGTCCAGGGCTCCTGAACACTACATAAAAC
 TGGCACAAGTAAGTCCCCTCCTCAAACCAACACAGGCAGTGTGTATGTGAGCACCTCGTG
 GGTGAGTATGTGTGGGCACAGGCTGGCTCCCTCAGCTCCACGTCTAGAGGGCTCCGA
 GGAGGTGGAACCTCAACCCAGCTGCGCAGGAGGCGGCTGCAGTCCTTCTCCCTCAAAG
 GTCTCCGACCCTCAGCTGGAGGCAGGCTGGCATTTCTAAAGGGTCCCCATAGGGTCTGGTTCC
 ACCCCATCCCAGGTCTGTTGAGGCAGGCTGGAGGGTCCCTACGATGGTTAGGGTGC
 ATGGAGGGCTGACTGCCACATTGCCTTCAGACAGGACACCGAGCATGAGGTAAGGCCGC
 CCTGACCTGGACTTCAGGGGAGGGGTAAGGGAGAGAGGAGGGGGCTAGGGGCTCT
 AGATCAGTGGGGCACTGCAGGTGGGCTCTCCCTACGATGGACACCTGCTGGATGTCAC
 CTCTGCAACCACACCCATGTGGTGGTTCATGAACAGACCACGCTCCTGCCTCTCCTGG
 CCTGGACACACAGAGCCACCCGGCCTGTGAGTGACCCAGAGAACGGAGGCCTCGGAGA
 AGGGTGCTCGTAAGCCAACACCAGCGTGCAGGCGCTGCACACCCCTCGGACATCCCAGGC
 ACGAGGGTGTGAGTGTGCCACACATAGGACCACACGTCCCAGCTGGAGGGAGAGGCCT
 GGGGCCCCCAGGGAGGGAGGCAGGGGTGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
 CCGCAGCCTGGTATGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
 TGGAAGATGCTGAGTGTCTCAAGCAGCAGTACGAGCAGCTGGGCTGCCAGGGCAAC
 GTGGGGGGGGAGACTCAGCTGGACAGCCCCTGCCTGTCACTCTGGAGCTGGCTGCTG
 CTCAGGACCCCTCTCCGACCCGGACAGAGCTGAGCTGGCCAGGGCAGGAGGGGGAGG
 GAGGGAATGGGGTGGCTGTGCGCAGCATCAGCGCCTGGCAGGTCCGAGAGCTGCGGG
 TGTGATTAAAGTCCCTGATGTTCTC

FIGURE 208

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
><subunit 1 of 1, 157 aa, 1 stop
><MW: 17681, pI: 7.65, NX(S/T): 1
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPIAKITREKLDQVATAVYQMMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP
```

Signal peptide:

amino acids 1-15

FIGURE 209

AGCAGGAGCAGGAGAGGGACA**ATG**GAAGCTGCCCGTCCAGGTCATGTTCTCTTATTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGCCTG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCAATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCTTCAGGATTAGAAATACCAGCAGTGCCCATACTCCA
 TAGCATGGTGCAAAAATTCCCAGGCGTGTCAATTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAAACATCACTGGAACACCCTGCCTCTTCGCCTGGTAGACAATGAACAACTG
 AATTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCAATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCCTGTGACTGTGATTGGGTTATTCAACAGCG
 TAATTCAAGATTCACTCCTCCTGATAATGAACAAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATAACCAGAAGGCAGCCAAGCTCTCCAGGGAAAGATTCTCTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTCAAACCTAAAGGAGTCTCAACTGCCAG
 CTTGGCAATTACCAAGACTCTAGATGACGAGTGGATACACTGCCACAGCAGAAGTTCC
 GTAGAGCATGTGCAAAACTTTGTGATGGATTCTTAAGTGGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**TGA**CTTCTCCTGGAACTACATATGCC
 AAGTATCTACTTATGCAAAGTAAAAGGCACAACACTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACACACACACACAGCAGCTCATTCTGTCTTAAATCTGTTTCTC
 TTCTCCTCTTTAAATTCAATCCTCACTCCCTATCCAATTCTCTTATCGTGCATT
 CATACTCTGTAAGCCCACACACACAGAGCTTCATTCTGTCTTAAAGGCTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCAATTGTCATTAAATATCAAGT
 TTGTATACTGCACATGACTTACACACAAACATAGTTCTGCTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTCTTCAAGCACATGTCGTCTGACTCAGGATAAAAACCAAAGG
 ATGGTTTAAACACCTTGTGAAATTGTCTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCCATGCTGGTTAGCATCTCCAACCTCC
 TATGTAATCAACAAACCTGCATAATAAAAGGCAATCATGTTATA

FIGURE 210

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLLFLLTCELAAEVAEVEKSSDGPAAQEPWTLDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRDVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMVTEYNPVTIVIGLFNSVIQIHLLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL
```

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGACCGGAGTGGGGAGCGCGCGGTGGAGGTGCCACCCGGCGCGGGTG
 GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
 GACGCGGCGGCGGGCGCGACTGCAGTGGCTGGACGA**TGG**CAGCGTCCGCCGGAGCCGG
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTCTGGCGCGCTTGG
 GCTCTTGACAGCTGGAGTATCAGCCTGGAAGTATATAGCCAAAAGAAATCTCGTGGCAA
 ATGGTACACAAGGAAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
 TCAGTCTCCTGGAGCTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTCCACTACTC
 CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAACAGCTGGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTATACACAATGGCACC
 TATATCTGTGATGTCAAAAACCCCTGACATCGTTGTCAGCCTGGACACATTAGGCTCTA
 TGTGCTAGAAAAAGAGAATTGCCTGTGTTCCAGTTGGGTAGTGGTGGCATAGTTACTG
 CTGTGGCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCTATAGAAGGAAA
 AACTCTAACGGATTACACTGGCTGCAGTACATCAGAGAGTTGTCACCAGTTAACAGGC
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGCTTGTAAAGAGTCTGCCTCTGGATCTCAC
 AGGGCCCAGTCATATATGCACAGTTAGACCCTCCGGCGGACATCACAGTGACAAGATTAAC
 AAGTCAGAGTCTGGGTGTATCGGATATCCGAAAGAAT**TAA**GAGAACACTAGAACATATC
 CTCAGCAAGAAACAAACAAACTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
 ACAAAAGGATATGTATAAATATTCTATTAGTCATCCTGATATGAGGAGCCAGTGTGCATGA
 TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTGCTGTTTGACTTTCTTT
 AGGTCAATTACAATTGGGAGATTTCAGAAACATTCCCTTCACCATCATTAGAAATGGTTG
 CCTTAATGGGAGACAATAGCAGATCCTGTAGTATTCCAGTAGACATGGCCTTTAATCTAAG
 GGCTTAAGACTGATTAGTCTTAGCATTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
 GCATACCCAGGGTGGCCTTACAGTACAGTACCTGATTTGTCTGCCCTTTAAAA
 AATACCCATTGGCTATGCCACTTGAAAACAATTGAGAAGTTTTGAAGTTTCTCACT
 AAAATATGGGCAATTGTTAGCCTTACATGTTGTAGACTTACCTTAAGTTGCACCCCTG
 AAATGTGTCATATCAATTCTGGATTCTAACAGTACAGTACCTGATTAAGTAAAGAAAATCCAAG
 GTCACCTCATTCTGGACACAGTGGATCAACTGATTAAGTAAAGTAAAGGATAAATGCCGAAG
 GAGAACTTTGTAAACGTGGAGAGTAAAAAGTATCGGTTTA

FIGURE 212

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAAALGLTAGVSALEVTPKEIFVANGTQGKLTCKFKST
TSTTGGLTSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDKKDASINIE
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWWVGIVTAVVLGLTLLISM
LAVLYRRKNSKRDYTGCSTSES LSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHSDKINKSESVVYADIRKN
```

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCTGTCAGCAGTGA
 CTGCCGGCTGGCCTCAAGCTGCGGACGACGCCGGTCCATCAGCGGCCGGCTGCCGCC
 TCTCGGCCACGGCTGGTCGGGGCCTCGGGCTGGGCTGGCGCTGGGTGAAGC
 TGGCAGGTGGGCTGAGGGCGCCGGCCCCGGCGAGTCCCCCGGGCCCCGACCCTGAGGCG
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTGCCCGTGGCTCCGCAGACCCGGC
 GCCGCCCTGCTCCAGGTGCTCGCCAGGCCATCGAGAGCAGCCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGCGCACCGGCATAGTGGTGGAGTTCTGTAGATGGAAAAGAAGTC
 TGGTCAGAAGGTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTGCTTTGCCAAATTGTGGGAAG
 CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTCTGTCACAACAAGATTACTGATTCCCATTAAAGTGGAAATTG
 TCATTATGAAAAGGACATAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTGAAGATGA
 TGAAAGAGAATGTTGCATTGAGCAAGAAAAGAAGGCAAAGTAATGAAAAGAATGATT
 ACTAAATTAAAACAGAGCAGGAGAATGAAGCCAATGCCGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTGAAACAAGGCGAATTATATTGAGAGAAAAGTTGAAAATTCAATTGAAT
 CCCTAAGATTATTTAAAAATGATCCTTGTCTCAACCTGGTAGTCAGTTTGATTCA
 ACTTTGGCTATACCCACTGGCAGCCATAGTAGAGAGAGCTCAGGATGTAATATTGGA
 CTATATGCAGAAAATATTCCATGACTGGATATGCTGACGACTGTGCAGGAAGAAACGAGC
 CAGTGATTACAATAGAGCAAGG**TAA**ATGAATACTTCTGCTGTCTAGCTATATCGC
 ATTAACACTATTTATTAATTAAAAGTCAAATTCTTGTCTCATCTGAAAGTGAAGGAAGTAA
 CACATTGGGAGCTTCTACATGTCTGTTCTCATCTGAAAGTGAAGGAAGTAAACA
 TGTTATAAAAGTAAAAAAA

FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQAGLPPLGHGWVGGLGLGLALGVLAGGLRG
AAPAQSPAAPPDPEASPLAEPPQEQLAPWSPQTAPPACSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLSLTVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKNDFEQGELYLREKFENSIESRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLTTQEENEPVIYNRAR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACCGTACGTAAGCTCGGAATTGGCTCG
AGGCTGGTGGAAAGAACGCCGAG**ATG**CGCCAGCCAGCGCTGGGCAACCCGGCTGCTCCTGC
TCTTGCTGATGGCGGTAGCAGCGCCCAGTCGAGCCGGGCAGCGCTGCCGGCCGGACT
GGTGCAGGAGGGCTGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGCTGCT
GCTGGAGCACTCATTGAGATCGATGACAGTGCCAATTCCGGAAGCAGGGCTCACTGCTCT
GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGGAGCAGGGC
CGACTCCGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCAAAGGCGACCCGG
GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTGTCCCTGCGTGCTCCCTGG
TGGAGTCGCACCTGTCGGACCAGCTGACCTGCACGTGGATGTGCCGGCAACGTGGTGGC
GTGTCGGTGGTGACGCACCCGGGGCTGCCGGGCCATGAGGTGGAGGACGTGGACCTGGA
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
CCTTCATTGAGCGCCTGGAGATGGAACAGGCCAGAAGGCAAGAACCCCCAGGAGCAGAAG
TCCTTCTCGCAAATACTGGATGTACATCATCCCGTCCTGTTCCCTCATGATGTCAGG
AGCGCCAGACACCGGGGCCAGGGTGGGGTGGGGTGGTGGTAGTGGCC
TTTGCTGTGCCACCCCTCCCTG**TAA**GTCTATTAAAAACATCGACGATACTGAAATGTG
TGAACGTTTGAAAAGCTACAGCTTCCAGCAGCCAAAGCAACTGTTGTTGGCAAGACGG
TCCTGATGTACAAGCTTGATTGAAATTCACTGCTCACTGATACGTTATTAGAAACCCAAG
GAATGGCTGTCCCCATCCTCATGTGGCTGTGGAGCTCAGCTGTGTTGTGGCAGTTAT
TAAACTGTCCCCAGATCGACACGCAAAAAAAA

FIGURE 216

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pi: 5.80, NX(S/T): 1
MAAASAGATRLLLLLMAVAAPSRARGSGCRAFTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLWNQQDGTLSLSQRQLSEERGLRDVAALNGLYRVRIPRPGALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEKSFFAKYWMYIIIPVVLFLMMMSGAPDTGGQ
GGGGGGGGGGSGLCCVPPSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCCGCAGACCGGGGCAGCAGGTGTCGTCGGGGGCCACC
ATGCTGGTGAUTGCCTACCTTGCTTTGTAGGCCTCCTGGCCTCCTGCCTGGGCTGGAACT
 GTCAAGATGCCGGCTAAACCCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTTCCTGGCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
 TGGCCTTGCCCTACAGTCCTCTTGCCCTAGTGGCCTCCTCCCTGTGGATTGGCTGGTC
 GCAAGAATTCTTGTGTCCTCTCCCTGACTTAUTCACTATGCTGCTAACCAAACCTCT
 CAAGACTACTTGTGCTGCTAGTGGGGCGAGCACATTGGTGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCCTGGTATATCCATGAGCACGTGGAACGGCATGACTCCCTGCTGAGT
 GGATCCCAGCTACCTTGCTCGAGCTGCCTCTGGAACCAGTGTGCTGGCTGTAGGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGCCTGTAGGCCCTTGTGGCTGC
 CATCCCTCTGGCTCTGGCAGGGCCCTGGCCCTTCGAAACTGGGGGAGAACTATGACC
 GGCAGCGTGCCTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCTGCGACCGCCGC
 GTGCTGCTGCTGGCACCATACAAGCTCTATTGAGAGTGTCACTTCATCTTGCTTCCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGCATTATCTCTCCAGCTTCATGG
 CAGCCAGCCTGCTGGCTCTCCGTACCGTATGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTGCTGTGCTCATCGTCGTTCTCTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTCATAGCCTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTCCCAGCATGAGCTTCCGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT
 CCTTGTCCCTCATGACAGTGATCGAAAAACAGGCACTCGAATATGTCAGCATTGCTCTG
 CTGTCATGGTGTGGCTCTGCTGGCAGTGGTGGACTCTCACCGTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTCACCTACTGAGGAGGCCATTGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGACAGACTCTGAATTCCAGCTATCCGGATTGTACAGATCTCTGT
 GACTGACTTGTGACTGTCTGTGGTTCTGCCATTGCTTGTGTTGGAGGACATGA
 TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTTCCCTCTGTGTTACTCCCATTAGAAA
 ATAAACACTTTAAATGATCAAAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAIFWNHVLA
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVI
PETEQAGVLNWFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAVVGLFTVVRHDA
ELRVPSPTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGGCGGGCGAGAGGAAACGCGGCCGGCCGGCCCTGGAG**ATG**
 GTCCCCGGCGCCGGCTGGTGTCTCGTCTGGCTCCCGCGTCGCGCCCA
 CGGCTTCCGTATCCATGATTATTGTACTTCAAGTGCTGAGTCCTGGGACATTGATA
 TCTTCACAGCCACACCTGCCAACGGACTTTGGTGTATCTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGAACTCAGCAACGGTTCTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGCTGCTCCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGTGATCATCTGACAACGCAGTTGACAATGACAGCTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTTCTGCTCGG
 CCGAGACGGCTACATGATCCGCCGCTCTGGAACAGCATGGGCTGCCATGGGCCATCATT
 CCATCCCAGTCAATGTACCAGCATCCCCACCTTGAGCTGCTGCAACCGCCCTGGACCTTC
TGGTAGAAGAGTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGAAACCC
 AGGAATTTGCTACTTGGATTGGAGATAGCATCTGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGGTTGGCGTTGCTAGGCTGAAAGGAAGCCACACCACTGGCCTCCCTCCCCAGG
 GCCCCCAAGGGTGTCTCATGCTACAAGAACAGAGGCAAGAGACAGGCCAGGGCTTCTGGCTA
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTACACT
 CACCTGGCTCCAGCCTCCCCACCCAGGGTCTCTGCACAGTGACCTCACAGCAGTTGTTGG
 AGTGGTTAAAGAGCTGGTGTGGGACTCAATAACCCCACTGACTTTAGCAATAAA
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAA

FIGURE 220

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW
```

Signal peptide:

amino acids 1-20

.....

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGGGCTGGTGGTGA
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG
AGGCCAACCAAAGATGCCACGGACTGGTGTGCCAGACCCATGACTGCTGCTATGACCACC
TGAAGACCCAGGGTGC GG CATCTACAAGGACAACAACAAAAGCAGCATACTATTGTATGGAT
TTATCTCAACGCTATTGTTAATGGCTGTGTTAATGTGATCTATCTGGAAAATGAGGACTC
CGAATAAAAAGCTATTACTAWTTNAAAAA
AA

FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pi: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGC
HCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVFNV
IYLENEDSE
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTCCTTCTGGATGGGGGCCAGGGGCCAGGAGAGTATAAAGGCATGTGGAG
GGTCCCCGGCACACCAGACGCCAGTCACAGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCTCCTGGGGGCCACCTGGCAGGAAGATGTAT
GCCCTGGAGGAGGCAAGTATTTCAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTCCTGGTAAAAGTGTCCAGGTGAAACTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGAAATACCCAGGAAGTCACCCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTGTCGCCTCCAAGCTTCCTCCGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTCATTTGGAAAGCTTGATGCCAGATCTCCTGCCTACCCCAGCCAAG
AGGGGCAGGTGCTGGTGGCATCTATGCCAGTATCAACTCCTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAACCTCACACTC
AGCAAACCTACCCGTGGTCGC**TAG**GGTGGGTATGGGCCATCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAAGTGAGTCGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTCTGCAGAAAA

FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
>subunit 1 of 1, 178 aa, 1 stop
>MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPAGGKYFSTTEDYDHEITGLRVSGLLLVKSVQVK
LGDSDVVKLGALGGNTQEVTLQPGEYITKVFVAFQAFRLRGMVMTSKDRYFYFGKLDGQISS
AYPSQEGOVLVGIYGOYOLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

Signal peptide:

amino acids 1-22

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCCTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAACTGGGTGCTCATCACGGGAAC TGCTGGCTATGGAATA CAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGCCTGGAAGAATA CACATGTTTCGATAAGAAGAAATTG TAGGATCCAGTT
 TTTTTTTAACCGCCCCCTCCCACCCCCCAAAAAACTGTAAGAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTGATGTTTGCTGCGAATGCGGTGTTGGGATT
 TATTGTTCTGGAGTGTCTGCGTGGCTGGCAAAGAATAATGTTCCA AAAATCGGCCATCT
 CCCAAGGGGTCCAATTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGGCTGTCATGCAACTGGCCCTAAGCCAAAGC AAAAGACCTAAGGACGACCTTGAA
 CAATACAAAGGATGGTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGTCTTACTGACAATGCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTGCTCCCTCGCTATAACAGCCTCAAAAACCTTAAGTATAAT
 CAATTTAAAGGGCTAACCGAGCTCACCTGGCTATACCTGACCATAACCATAACGCAATAT
 TGACGAAAATGCTTTAATGGAATA CGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
 TCTCCTATTCTTAACAATACCTTCAGACCTGTGACAAATTACGGAAC TTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGGATCTGAAACAGTTCCGGGCTTGC GGAAAGCTGCTGAGTT
 ACATTTACGGTCTA ACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC
 TGGAACTTTGGACCTGGGATATAACCGGATCCGAAGTTAGCCAGGAATGTCTTGCTGGC
 ATGATCAGACTCAAAGAAACTTCACCTGGAGCACAATCAATTTCAGCTCAACCTGGCCCT
 TTTCCAAGGTTGGTCAGCCTTCAGAACCTTACTTGCA GTGGAATAAAATCAGTGTCA TAG
 GACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTATCAGGCAATGAGATC
 GAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGTCCGAATCTGCAGCCCTAACCTGGG
 TTCCAACAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACA
 TCAGTCTGCTGGGAATATGGGAATGCAGCAGAAATATTGCTCCCTGTAAACTGGCTG
 AAAAGTTAAAGGTCTAAGGGAGAATA CAAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGT
 TTGATCTGCCAGGGCTCTCCAAAGCCGACGTTAACGCCAAGCTCCCCAGGCCAGACCGATGC
 GAGAGCAAACCCCCTTGCCCGACGGTGGAGCCACAGAGCCGGCCAGAGACCGATGC
 TGACGCCGAGCACATCTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTCTGTCCG
 TGCTCGTCATCCTGCTGGTTATCTACGTGTATGGAGCGGTACCCCTGCGAGCATGAAGCAG
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT
 GACTCCCAGCACCCAGGAATT TATGTAGATTATAAACCCACCAACCGAGACCGAG
 TGCTGCTGAATGGGACGGGACCCCTGCACCTATAACAAATGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTAAAGCTGGGAATAAGTGGTGTCTTATTGAACTC
 TGGTGACTATCAAGGGAACCGCGATGCCCTCCCTCCCTCCCTCACTTGGTGG
 CAAGATCCTCCTGTCCGTTAGTCATTATAACTGGTCACTTCCCTCTCATACATA
 ATCAACCCATTGAAATTAAATACCAACATCAATGTGAAGCTTGAACCTCCGGTTAATATAA
 TACCTATTGTATAAGACCCTTACTGATTCCATTAATGTCGCA TTGTTAAGATAAAACT
 TCTTCATAGGTAAAAAAAAAAA

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKELHLEHNQFSKLNLAFLPRLVSLONLYLQWNKISVIGQTM
SWTWSSLQRDLDSGNEIEAFSGPSVFQCVPNLQRLNLDNSNKLTFIGQEILDWSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELGQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCC
 TAAATATGTCAAGATCCAGACTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
 TGTTGCCGCTATTCCAGTTGGTCTCGGACCTACCAGTCGAAGAAGATGAAATGTGT
 AAATTATAATGACCAACACCCCTAATGGCTGGTATATCTGGATCCTCCTGCTGGTTTGG
 TGGCAGCTCTCTGTGGAGCTGTGGCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCGA
 ATTGATTCTCACAGGCGCACCATGGCAGTTTGCTGGAGACTGGACTCTATTATGG
 GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTCAAACACTAAACCCCTGACCTAT
 ATCCTGTTCCATGCTCCATGTTGGCCCTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
 AAAACAACTGATTTAGGTGTGGATTATCAATTAAAGTATTAACGACATCTGTAATTCCA
 AACATCAAATTAGGAATAGTTATTCAAGTGTGGAAATGTCCAGAGATCTATTCA
 GTCTGAGGAAGGACAATTGACAAAAGAATGGATGTTGGAAAAAATTTGGTCA
 TGGAGATGTTAAATAGTAAAGTAGCAGGCTTGATGTGCACTGCTGTATCATA
 CTTTACACTTACAGTCCACTGCAGTACAGCACACCATTCTGCTTAAACTCTTC
 CTAGCATGGGTCCATAAAATTATAATTAAACAATAGCCCAAGCCGAGAATCCA
 AACATGTCCAGAACCAAGAACAGAAAGATAGTATTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTGGAGTTGAAGGGTAAAGGATAATGAAGAGGAAAGGAAAGATTACAAGTCT
 CAGCAAAACAAGAGGTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGACATATAATGCCAACACGGGAGAAAAGAAAATTCCC
 CTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTG
 GCATTATTGCAGCATCATGCTAAGAACCTCGGCATAGGTATCTGTTCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTCAAGTGGATTGGCAGTGGCCATCAGCAGGGGACAGA
 CAAAAACATCCATCACAGATGACATATGATCTCAGCTGACAAATTGTTGAACAAAACAAT
 AACATCAATAGATATCTAAAAA

FIGURE 228

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCEEDEMCVNNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAGDLDIYGTEAAVSPVGHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT
```

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTCGCCAGTGTGGGACGCAGCTGACGCCGCTTATT
 GCTCTCGCTCGCGCCCCGGCTCAGAAGCTCCGTGGCGCGACCGTGACGAGAACCCC
 ACGGCCAGCTCAGTTCTTCTACTTTGGGAGAGAGAGAGAAAGTCAGATGCCCTTTAAACT
 CCCTCTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATAACAACCTTGCTGAAG
 ATGAAGAATATACAATATTGAGGATAAATTTTTCTTTTCAAGTCTGATTGTGGC
 TTACCTCAAGTTACCATTTTCAGTCAGTCAAGTCTGTTGTTGCTTCTTCAGAA**ATG**TTTTTA
 CAATCTCAAGAAAAATATGTCCCAGAAATTGAGTTACTGTTGCTTGTATTGGACTCATT
 TGGGGATTGATGTTACTGCACTATACTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA
 ACACAGTGGATGTCGAGAACGGTGCTCTATGGCAGGATATGCGGATCTGAAAAGAACAAATT
 GCTGTCCTCTGGATGACATTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGAAATTGGTGCCAGTAA
 CCACAAATAAAAGAACGAATGTCGGGCAGTATCAGA**TAG**CAGTTGAAAATCACCTTGTGC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTATAATTGCTGGCTTAGGAC
 AGAGCAATACTTTACAATAAAAGCTCTACACATTTCAGGAGTATGCTGGATTATGGAAC
 TCTAATTCTGTACATAAAATTAAAGTTATTGTTGCTTCAGGCAAGTCTGTTCAATG
 CTGTACTATGTCCTTAAAGAGAATTGGTAACCTGGTTGATGTGGTAAGCAGATAGGTGAGT
 TTTGTATAAAATCTTTGTGTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATT
 ATTCTATAACACATTATTTAAGTATATAACACGTTTTGGACAAGTGAAGAATGTTAA
 TCATTCTGTCATTGTTCTCAATAGATGTAACCTGTTAGACTACGGCTATTGAAAAAAATGTG
 CTTATTGTACTATATTGTTATTCCAATTATGAGCAGAGAACAGGAAATATAATGTTGAAAA
 TAATGTTGAAATCATGACCCAAAGAACATGTATTGATTGACTATCCTTCAGAATAACTGA
 AGGTTAATTATTGTATATTAAAAATTACACTTATAAGAGTATAATCTGAAATGGGTAG
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTAAATAACAGCATTAAAGCT
 GTAAACTCTAATCTTAACTTATTGAAGAACAAAGATATTGATGAGAGTAACAATA
 AAGTATTGATTTTCACATACATGAATGTTCAATTAAAGTTAATCCTTGAGTGTCT
 ATGCTATCAGGAAAGCACATTATTCCATATTGGTTAATTGCTTATTATATTGGTC
 TAGGAGGAAGGGACTTGGAGAATGGAACCTTGAGGACTTAGCCAGGTGTATAATAAAA
 GGTACTTTGTGCTGCATTAATTGCTGGAAAGTGTAAACATTATATTATAAGAGTATC
 CTTATGAAATTGATAACAGATGCATTAGATATTCAATTATATAATGCCAC
 TTAAAATAAGAACATTAAAGTATAAAACTATGAAGAGATTGACTATCTTTCAGGAAAAAGCT
 GTATATAGCACAGGGAACCCCTAATCTGGGTAAATTCTAGTATAAAACAAATTATACTTTAT
 TAAATTTCCCTGTAGCAATCTAATTGCCACATGGTGCCTATATTCTAGTATT
 CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTAGATTAGACTATATAGAATTAGATAT
 TGTATTGTTCGTCATTATAATATGCTACCACATGTAGCAATAATTACAATTGTTATTAAAA
 TAAATATGTGAAATTGTTCATGAAAGACAGATTCCAATCTCTCTCTGT
 CTGTCTACCTTATGTGAAGAAATTAAATTATGCCATTGCCAGGT

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
```

Important features of the protein:

Signal peptide:

amino acids 1-26

FIGURE 231

CGCGGGCCGGGCGCCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCAAGCCCCCAC
CATGCCTGGCCCCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAACCGGCCATGCT
TCCCCGGGTGCCAATGCAGGGTGGAGACCTCGGCCTTTCGACAGCTCAGCCTGACTCGG
GTGGATTGTAGCGGCCTGGGCCACATCATGCCGTGCCATCCCTCTGGACACAGCCA
CTTGGACCTGTCCCAACCAGCTGGAGATGGTAATGAGTCGGTGTGGCGGGGCCGGCT
ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCACTGCC
TTCTCCCGCCTCGCTACCTGGAGTCGCTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
AGCCGAGAGCTCACCACTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGGG
AGGTCTCAGTGTCTGCCTCACGACGACAGTCAGGGCCGGCACTACACGTGGACCTCTCC
CACAACTCATCACCGCCTCGTGCCTCACCGAGGGCCGGCTGCCTGCGCCCACCAT
TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC
TGCCTACCTGAGCCTGGATGGAACCCCTCTAGCTGTCTAGCTGCTTCGGGTGCCTCGCGGGG
CTGGGAGGCCTTACACACCTGTCTGGCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCCAG
TGGCTCCGTGAGCTACCAGGCTGCAGGTCTGGACCTGTCGGGCAACCCCAAGCTTAAC
GGGCAGGAGCTGAGGTGTTTCAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTCGGGCAAC
AACCTGGTCCCCCTGCCTGAGGCCTGCTCCTCACCTCCGGCACTGCAGAGCGTCAGCGT
GGGCCAGGATGTGCGGTGCCGGCCTGGTGCAGGGCACCTACCCCCGGAGGCCTGGCT
CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGAAATCTGCTGCCAGGGCCCCACC
ATCTTG**TGA**CAAATGGTGTGGCCAGGGCACATAACAGACTGCTGCTGGCTGCCTCAG
GTCCCAGTAACTTATGTTCAATGTGCCAACACCAGTGGGAGCCCGAGGCCTATGTGGCA
GCGTCACCACAGGAGTTGTGGCCTAGGAGAGGCTTGGACCTGGGAGGCCACACCTAGGAGC
AAAGTCTCACCCCTTGTCTACGTTCTCCCCAACCATGAGCAGAGGACTTCGATGCCA
AACCAAGACTCGGGTCCCCCTGCTTCCCCACTTATCCCCAACGTGCCCTCCCTCAT
GCCTGGCCGGCTGACCGCAATGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA
GTTCAGGTCACTGGCTGAGTGTCCCCCTGGGCCATGGCCAGTCACTCAGGGCGAGTT
TCTTTCTAACATAGCCCTTCTTGCCATGAGGCCATGAGGCCGCTTCATCTTTCTAT
TTCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCCTCATGTGAC
AGATGGGAAACTGAGGCCTTGAGAAGGAAAAGGCTAATCTAACGTTCTGGGGCAGTGGC
ATGACTGGAGCACAGCCTCTGCCCTCCAGCCGGACCCAATGCACCTTCTGTCTCCTCTA
ATAAGCCCCACCCCTCCCCGCTGGCTCCCCCTGCTGCCCTGCCTGTCCTCCTCATAGCACA
GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAAGTGGACTCTGGGCTCTGACCAGCT
GTGCAGGCTAAGTCACTCTGCCCTCGGAGCCTCTGGAGCCTAGGGCACATTGGTT
CCAGCCTAGCCAGTTCTCACCCGGTTGGGTCCCCCAGCATCCAGACTGAAACCTACC
CATTTCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA
TCTGGCTGGGATCTCCAAGGGCCTCTGGATTAGTCCAGTCCCCACTGGCCCTGAGCACGACAGC
CCTCTTACCCCTCCAGGAATGCCGTGAAAGGAGACAAGGCTGCCGACCCATGTCTATGC
TCTACCCCCAGGGCAGCAGTCAGCTGCCGAACCTGGCTGTTCTTAGTCTCATTTA
TAAAAGTTGTTGCCTTTAACGGAGTGTCACTTCAACCGGCCCTCCCTACCCCTGCTGGC
CGGGGATGGAGACATGTCATTGTAAAAGCAGAAAAAGGTTGCATTGTTCACTTTGTAAAT
ATTGTCCTGGGCTGTGTTGGGGTGTGGGGGAAGCTGGGATCAGTGGCCACATGGGATC
AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTGTCTTCCCCACCTGCCTAGC
CCATCATCTAACGGCTCTGATTAAACACTATAAAAGGTTAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLAVSGAQQTTRPCFPQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHVDSLHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRQLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRPELAPS
GFRELPGQVLSDLGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVSV
GQDVRCRRLVREGTYPRRPQSSPKVPLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTCTGTGAGATTGATTCGATTCTCCCCAGTTCCCCTGTGGGTCTGAGG
 GGACCAGAAGGGT GAGCTACGTTGGCTTCTGGAAGGGGAGGCTAT**ATGCGTCAATTCCCCA**
 AAACAAGTTTGACATTCCCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCCTGCT
 GTTCCAGGCCTTACCTGCTGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTCTTCA
 GGGAGGCTTGGCAGTTTCTTACTCCTGTGGTCTCCAGATTCAGGCCTAAGATGAAAGCC
 TCTAGTCTTGCCTCAGCCTCTCTGCTGCCTTATCTCCTATGGACTCCTCCACTGG
 ACTGAAGACACTCAATTGGGAAGCTGTGATGCCACAAACCTTCAGGAAATACGAAATG
 GATTTCTGAGATA CGGGGAGTGTGCAAGCAAAGATGGAAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCGCCATT
 GCTAAGACTCTATCTGGACAGGGTATTAAAAACTACCAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTGCCAATTCTTCTTACCATCAAGAAGGACCTCCGGCTCTCAT
 GCCCACATGACATGCCATTGTGGGAGGAAGCAATGAAGAAATACAGCCAGATTGTGAGTCA
 CTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTGGGGAACTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAA**TAGGAGGAAAGT**GATGCTGCTGCTAAGAATATTGAGGT
 CAAGAGCTCCAGTCTCAATACTGCAGAGGAGGCATGACCCAAACCACCATCTCTTACT
 GTACTAGTCTGTGCTGGTCACAGTGTATCTTATTGCTTACATTGCTTGCATGAT
 TGTCTTATGCATCCCAATCTTAATTGAGACCATACTGTATAAGATTTGTAATATCTT
 TCTGCTATTGGATATTTATTAGTTAATATTTATTATTGCTATTAAATGTATT
 ATTTTTTACTTGGACATGAAACTTAAAAAAATTCAACAGATTATTTATAACCTGACTAG
 AGCAGGTGATGTATTATACAGTAAAAAAAAACCTTGTAAATTCTAGAAGAGTGGCT
 AGGGGGTTATTCAATTGTATTCAACTAAGGACATATTACTCATGCTGATGCTGTGAGA
 TATTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTGATGTGGAATT
 GCACATCTACCTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATATTGTGTAT
 CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAAGTTTCTTGCATA
 CCAAAAAAAAAAAAAAAA

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRILYLDRVFKNYQTP
DHYTLRKISSLANSFLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVVKALG
ELDILLQWMEETE
```

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCCTACTGCTGA**ATG**TCCGTCCGGAGGAGGGAGGCTTTGCCG
 CTGACCCAGAGATGCCCGAGCGAGCAAATTCTACTGTCCGGCTGCAGGCTACCGTGGC
 CGAGCTAGCAACCTTCCCCTGGATCTCACAAAAACTCGACTCCAATGCAAGGAGAACAG
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCTATAGGGGAATGGTGCACACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
 TGTTGGCAAAAGTGAAGATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATG
 GCTGGTGTATTGGCCAGTTTAGCCAATCCAACGTGACCTAGTGAAGGTTCAGATGCAAAT
 GGAAGGAAAAAGGAAACTGGAAGGAAAACCATTGCGATTCGTGGTACATCATGCATTG
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTGGCAGGCTGGTACCCAATATAACAA
 AGAGCAGCACTGGTGAATATGGGAGATTAAACCACTTATGATACTGAAACACTACTTGGT
 ATTGAATAACCACTTGAGGACAATATCATGACTCACGGTTATCAAGTTATGTTCTGGAC
 TGGTAGCTTCTATTCTGGAACACCAGCGATGTCATCAAAGCAGAATAATGAATCAACCA
 CGAGATAAACAGGAAGGGACTTTGTATAAATCATCGACTGACTGCTTGATTCAAGCTGT
 TCAAGGTGAAGGATTCATGAGTCTATATAAGGCTTTACCATCTGGCTGAGAATGACCC
 CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTT**TAA**

FIGURE 236

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pi: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDA
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLEVVFGKSEDEH
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCGLVASILGTP
ADVIKSrimnQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRTMPWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTCCTGCAGCG
 GCCTGAAGTCGGCGTGGCGTTGAGGAAGCTGGATAACAGCATTAAATGAAAAATTATGC
 TTAAGAAGTAAAA**ATG**GCAGGCTCCTAGATAATTCGTTGGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAATGCTGTGCATCTGTTGTCGCAGGTATATTGTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAACGCCAGAACAGTTGAACCAGCCTT
 TCACACATGTGGTGATTTCCACATTGGCTTCTCATGATAAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTAGGAAGAACAGGTGCTCGAGTTGGCTT
 TTCATTGGTTCATGTTGATGTTGGTCACTTATTGCTTCCATGTGGATTCTTTGGTGC
 ATATGTTACCCAAAATCTGATGTTATCCGGGACTAGCTGTGTTTCAAAATGCACTTA
 TATTTTTAGCACTCTGATCACAAATTGGAAGAACCGAAGAGCTATGGACC**TGA**GATCAC
 TTCTTAAGTCACATTTCTTGTATATTCTGTTGAGATAGGTTTATCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTGTTCTTACATTTATGTC
 TGAGTTTGAAATAGTTATGAAATTCTTATTTTCATTGCATAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTATTCCCTGAGATTAGAA
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTGTCATTTAGAAGTAACCACCTTGT
 CTCTCTGGCTGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTGGGAGGCCAGGG
 CCGATTGCTTGAGGTCAAGTGTGAGACCAGCCTGGCCAACATGGCGAAACCCATCTACT
 AAAAATACAAAATAGCCAGGCATGGTGGTGGTGCCTGTAATCCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAATCGCTGAACCCGGGGGCAGAGGTTGCAGTGAGCTGAGTTGCGCCAC
 TGCACCTAGCCTGGGGAGAAAGTGAAAACTCCCTCTCAAAAAAAAGACCACTCTCAGTATC
 TCTGATTCTGAAGATGTACAAAAAAATAGCTTCATATATCTGGAATGAGCACTGAGCCA
 TAAAAGGTTTCAGCAAGTGTAACTTATTTGGCTAAAATGAGGTTTTGGTAAAGA
 AAAAATATTGTTCTATGTATTGAAGAAGTGTACTTTATATAATGATTAAATGCC
 AAAGGACTAGTTGAAAGCTCTTTAAAAAGAATTCCCTCAATATGACTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWWIMIDAAVVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFGRTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGCCCGCAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGACTGTCAGAAGCTGGCCAGGGTGGT
 GGTCAAGCTGGTCAGGGACCTACGGCACCTGCTGGACCACCTCGCCTCTCCATCGAACAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAAGCTGACCCCAAGCCACCCCTCACCTGGACAG
GATGAGAGTGTCAAGGTGTGCTCGCCTCGGCCCTCATCTTGCCATAGTCACGACATGGA
 TGTTTATTCAAGCTACATGAGCTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCACCAAGGAGATCCAGGTTAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACTAACCTTGCGTTAAAATCTGCAGTGGGCCCAACGTCGTGGCCCTACTATGT
 GCTTGAAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGCAGAGGCCTAACATC
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCTTAAAGAAATTCCGGGGGTGCACTGGTGTGGTGG
 CCTCCTACGACGATCCAGGGACAAAATGAACGATGAAAGCAGGAAACTCTCTGACTTG
 GGGAGTTCTACGCAAAACAACGGGCTCCGGGACAGCTGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGTAAAAGCCCCTTGAGCAGTTCTAAAGAACAGCCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGGAGATGGAGGGCTGCATGCCCGAAGCCATTTTAGGGTGGC
 TGTGGCTCTCCTCAGCCAGGGCCTGAAGAACGCTCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGCTGAGGAGGAGGAGCAGGGGTGCTGCGTGGAAAGGTGCTGCAGGTCTGCACGC
 TGTGTCGCGCCTCTCCTCGGAAACAGAACCCCTCCACAGCACATCCTACCCGGAAGACC
 AGCCTCAGAGGGCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGTGCTTCGTCAGGG
 ACTGCTGACGGCTGGCCTGAGGAAGGACAAACTGCCAGACTTGAGCCAAATTAAATTAA
 TTTTGCTGGTTTGAAAAAAAAAAAAAA

FIGURE 240

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
MRVSGVLILLALIFAIVTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPKPF
```

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCCTGGGGAT
 CCAGAAACCCATGATAACCCTACTGAACACCGAATCCCCTGGAAGGCCACAGAGACAGAGACA
 GCAAGAGAACGAGATAAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCAGTCCC
 CTGCACCCCTTCCTGGGACACT**ATG**TTGTTCTCCGCCCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCA
 GCCTCTTACCCCTGAGTGTGAAACAATGCCAGTCGCCATCGATATTAGACAGACAGTGT
 GACATTGACCCCTGATTGCCTGCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC
 CTTGGACCTGCACAACAATGCCACACAGTCAACTCTCTGCCCTTACCCGTATCTG
 GGTGGACTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGTGAGAAAGGATC
 CCCAGGGGGTCAAAACACCAGATCAACAGTGAAGCCACATTGCAAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCTGGCT
 GTCTGGCATCCTAATTGAGGTGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTCAACCTAACAGAG
 AGCTGCTCCCCAACAGCTGGGCAGTACTTCCGCTACAATGGCTCGCTACAACACTCCCCCT
 TGCTACCAAGAGTGTGCTCTGGACAGTTTTATAGAAGGTCCCAGATTCAATGGAACAGCT
 GGAAAAGCTTCAGGGACATTGTTCTCCACAGAAGAGGAGCCCTTAAGCTCTGGTACAGA
 ACTACCGAGCCCTCAGCCTCTCAATCAGCGCATGGCTTGTCTTCACTTCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTGGTTGGCTGTCTG
 CCTCTCCTGGCTTTATTCATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGCTTCACCTCAGCACAAGCCACGACTGAGGCA**TAA**ATTCTCTCAGATACCA
 TGGATGTGGATGACTCCCTCATGCCTATCAGGAAGCCTCTAAAATGGGTGAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCCTGGACATCTCTAGAGAG
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTCAGCCTCTCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTAATGCAGAGANCAAACCTCTGTTAGTTGCAGGG
 GAAGTTGGATATACCCCAAAGTCCTCTACCCCTCACTTTATGCCCTTCCCTAGATA
 TACTGCGGGATCTCTCCTAGGATAAAGAGTTGCTGTTGAAGTTGTATTTTGATCAATA
 TATTGGAAATTAAAGTTCTGACTTT

FIGURE 242

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pi: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTPPCYQSVLWTVFYRRSQISMEQLEKLQGTL
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLIPLTQM
LTIGPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPFVTQLGAQGTILSSEE
LPQIIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGT PAGRLPTPSG
TDDDFAVTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 245

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCAGCGGGCTCGGAGCGCGGCG
 GAGCCAGACGCTGACCACGTTCCCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCG
 GCAGCCGGGAGCC**ATG**CGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCC
 TGCTGCTCCTGCTGCTGCAGCTGCCCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCCTGGTCAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG
 GGATCCCAGGTGGGATGGATTCAAAGGAGAAAAGGGGAATGTCAGGGAAAGCTTGAG
 GAGTCCTGGACACCCAACACTACAAGCAGTGGTCAATTGAATTATGGCATAGATCT
 TGGGAAAATTGCGGAGTGTACATTACAAAGATGCGTTCAAATAGTGCTCTAACAGAGTTTGT
 TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTCACATT
 AATGGAGCTGAATGTTAGGACCTCTCCCATTGAAGCTATAATTATTGGACCAAGGAAG
 CCCTGAAATGAATTCAACAATTAATATTGACACTTCTTCTGTGGAAGGACTTGTGAAG
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGTTGGCACTGTTCAAGATTACCCAAA
 GGAGATGCTCTACTGGATGAAATTGAGTTCTCGCATCATTATTGAAGAACTACCAAA**TA**
AATGCTTTAATTTCTTGTACCTCTTTTATTATGCCTGGAATGGTCACCTAAAT
 GACATTAAATAAGTTATGTATACTGAAATGAAAAGCAAAGCTAAATATGTTACAGA
 CCAAAGTGTGATTCACACTGTTAAATCTAGCATTATTGCTTCAATCAAAGT
 GGTTCAATATTTTTAGTGGTTAGAATACTTCTTCAGTCACATTCTCTAACCTA
 TAATTGGAATATTGTTGTTGGCTTTGTTCTCTAGTATAGCATTAAAAAAATA
 TAAAAGCTACCAATCTTGTACAATTGTAAGAATTTTTATATCTGTTAAAT
 AAAAATTATTCCAACA

FIGURE 246

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pi: 8.43, NX(S/T): 1
MRPQGPAAASPQRRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217